

2 32
CTT TCA GAA GCC CGG GAG AGC GTC TTG GGG GAT TTG CTG AAG GTT GTG CTG TAC AGC CTG
leu ser glu ala arg glu ser val leu gly asp leu leu lys val val leu tyr ser leu

62 92
GGC AGT GCC CAG AGT GCC CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG AGG GCC CTT GTG
gly ser ala gln ser ala leu phe leu gln his gly leu ala thr gln arg ala leu val

122 152
TCC AAG TTC CCG GAG CTG CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC GAC CTG TGC CTG
ser lys phe pro glu leu leu phe glu glu asp thr glu leu cys ala asp leu cys leu

182 212
AGG CTC CTA CGA CAC TGT GGC AGC CGC ATC AGC ACC ATC CGC ACG CAC GCC AGC GCC TCG
arg leu leu arg his cys gly ser arg ile ser thr ile arg thr his ala ser ala ser

242 272
CTG TAC CTG CTC ATG CGA CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC CGT GTG AAG ATG
leu tyr leu leu met arg gln asn phe glu ile gly his asn phe ala arg val lys met

302 332
CAG GTC ACC ATG TCT CTC TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC AGT GAA GAG CAC
gln val thr met ser leu ser ser leu val gly thr thr gln asn phe ser glu glu his

362 392
CTG CGA CGT TCA CTC AAA ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG GGG CTG CGG GAC
leu arg arg ser leu lys thr ile leu thr tyr ala glu glu asp met gly leu arg asp

422 452
AGC ACC TTC GCA GAG CAG GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG ATC CTG ACG GAC
ser thr phe ala glu gln val gln asp leu met phe asn leu his met ile leu thr asp

482 512
ACG GTG AAG ATG AAG GAA CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC CTC ATG TAC AGA
thr val lys met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg

542 572
ATT GCC CGG GGC TAC CAG GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG CAG AAC ATG GCC
ile ala arg gly tyr gln gly ser pro asp leu arg leu thr trp leu gln asn met ala

602 |xxxxxxxxxxxxxxxx transmembrane domain xxxxxxxxxxxx
GGG AAG CAC GCG GAG CTG GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG GTG CAC GCG GCC
gly lys his ala glu leu gly asn his ala glu ala ala gln cys met val his ala ala

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx| 692
GCC CTC GTG GCT GAG TAC CTC GCC CTG CTC GAG GAC CAC CGC CAC CTG CCC GTG GGC TGC
ala leu val ala glu tyr leu ala leu leu glu asp his arg his leu pro val gly cys

722 752
GTT TCC TTC CAG AAC ATC TCA TCC AAT GTG CTA GAG GAG TCC GCC ATC TCC GAC GAC ATC
val ser phe gln asn ile ser ser asn val leu glu glu ser ala ile ser asp asp ile

782 812
CTG TCG CCC GAC GAG GAG GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG CTG GGG CTG GTA
leu ser pro asp glu glu gly phe cys ser gly lys his phe thr glu leu gly leu val

842 872
GGG TTG CTG GAA CAG GCA GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC GAG GCG GTG AAT
gly leu leu glu gln ala ala gly tyr phe thr met gly gly leu tyr glu ala val asn

FIG. 1 (1 of 3)

```

902                               932
GAG GTC TAC AAG AAC CTC ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC AAG AAG CTG GCC
glu val tyr lys asn leu ile pro ile leu glu ala his arg asp tyr lys lys leu ala

962                               992
GCG GTG CAC GGC AAA CTG CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG AGT TCC GGC TGG
ala val his gly lys leu gln glu ala phe thr lys ile met his gln ser ser gly trp

1022                               |xxxxx ITAM xxxx|1052
GAG CGC GTG TTC GGG ACG TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC TTC GGT GAC CTG
glu arg val phe gly thr tyr phe arg val gly phe tyr gly ala his phe gly asp leu

1082                               1112
GAT GAG CAG GAG TTT GTG TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA GAG ATC TCA CAC
asp glu gln glu phe val tyr lys glu pro ser ile thr lys leu ala glu ile ser his

1142                               1172
CGG CTG GAG GAG TTC TAC ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG ATT ATC AAA GAC
arg leu glu glu phe tyr thr glu arg phe gly asp asp val val glu ile ile lys asp

1202                               1232
TCT TAC CCT GTG GAC AAG TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC CAG ATC ACG TAT
ser tyr pro val asp lys ser lys leu asp ser gln lys ala tyr ile gln ile thr tyr

1262                               1292
GTG GAA CCG TAC TTT GAT ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC TTT GAC CGC AAC
val glu pro tyr phe asp thr tyr glu leu lys asp arg val thr tyr phe asp arg asn

1322                               1352
TAT GGG CTT CGC ACA TTC CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG CGC GCA CAC GGG
tyr gly leu arg thr phe leu phe cys thr pro phe thr pro asp gly arg ala his gly

1382                               1412
GAG CTG CCC GAG CAA CAC AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC GCC TTC CCC TAC
glu leu pro glu gln his lys arg lys thr leu leu ser thr asp his ala phe pro tyr

1442                               1472                               |xxxxxxxxxxxx
ATC AAG ACT CGC ATC CGT GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG CCA GTG GAG GTG
ile lys thr arg ile arg val cys his arg glu glu thr val leu thr pro val glu val

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GCC ATC GAG GAC ATG CAG AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC GAG CAG GAC CCA
ala ile glu asp met gln lys lys thr arg glu leu ala phe ala thr glu gln asp pro

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|
CCA GAT GCT AAG ATG CTA CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC ACC GTG AAC CAG
pro asp ala lys met leu gln met val leu gln gly ser val gly pro thr val asn gln

1622                               1652
GGT CCC CTG GAG GTG GCC CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC CCC AAG CTC TTC
gly pro leu glu val ala gln val phe leu ala glu ile pro glu asp pro lys leu phe

1682                               1712
CGG CAT CAC AAC AAA TTG CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA TGT GAG GAT GCG
arg his his asn lys leu arg leu cys phe lys asp phe cys lys lys cys glu asp ala

|xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
CTG CGG AAA AAT AAG GCC CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC CGT GAG CTG GAG
leu arg lys asn lys ala leu ile gly pro asp gln lys glu tyr his arg glu leu glu

```

FIG. 1 (2 of 3)

```

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX!
CGC AAC TAC TGC CGC CTG CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG CGC CTG CCC CAG
arg asn tyr cys arg leu arg glu ala leu gln pro leu leu thr gln arg leu pro gln

1862                                1892
CTG ATG GCA CCC ACC CCA CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA AGT TTC CGA AAG
leu met ala pro thr pro pro gly leu arg asn ser leu asn arg ala ser phe arg lys

1922                                1952
GCA GAC CTC TGA GCC CAC AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG CAC CCG GGC CTC
ala asp leu STP

1982                                2012
AGC TGT CTG TGC TGC GAG GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT GGG GTG ACC ACA

2042                                2072
CTG TAC TTG GGG CTG GGC CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA CTG ATG CTT CCT

2102                                2132
CCC TTT TTT AAT TTA AAA TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA

```

09736568-107607

FIG. 1 (3 of 3)

102101" 8969E/60

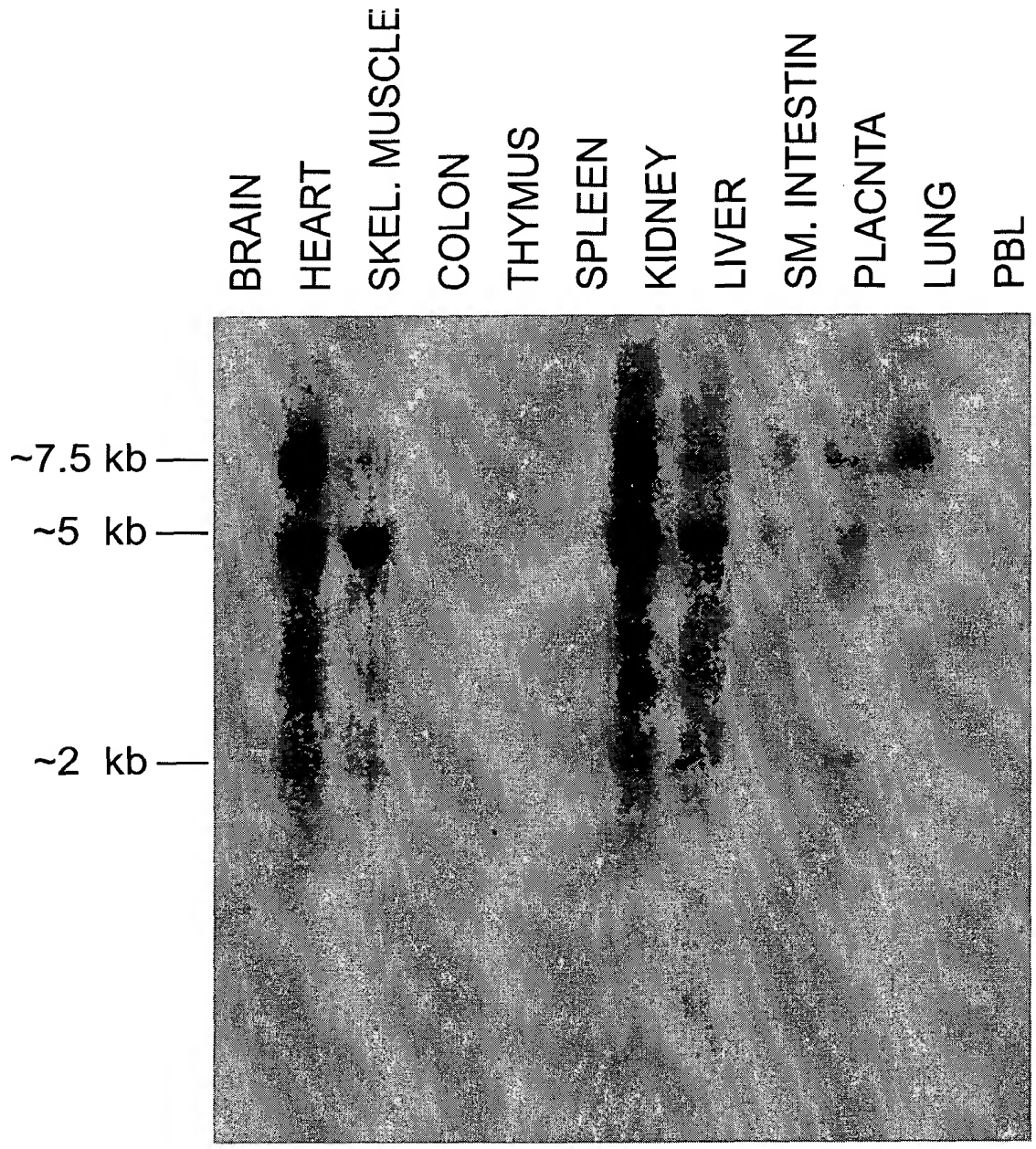


FIG. 2

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPFEYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSFAFAVLHHHQNPFEYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWLVPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPSPDDEVRSIIGSKGLDRSNSWNTGGPKAAPWGSNPSPSAES
HC5	-----

FIG. 3A (1 of 5)

HC2A	I IHVVAQCHEEGLESHLSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
KIAA	I IHVVAQCHEEGLESHLSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
rat	-----
HC4	LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN
HC1	LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK
HC3	TQAMDRSCNRMSSHTETSSFLQTLTGRLP----TKKLFHEELALQWVVCSG--SVR---E
HC5	-----
	Cadherin Cleavage
HC2A	KLLRYSWFFFDVLIKSMQHLIENSKVKLIIRNQRFPASYHHAAETVVNMLMPHITQKFGD
KIAA	KLLKYSWFFFDVLIKSMQHLIENSKVKLIIRNQRFPASYHHAAETVVNMLMPHITQKFRD
rat	-----
HC4	KLLKYSWFFFEIIAKSMATYLLIENKIKLTHGQRFPPKAYHHALHSLFLAIT-IVESQYAE
HC1	HVLKHSWFFFAIIILKSMQHLIDTNKIQLERPQRFPEQNELDNLMVLSHDHVIWKYKD
HC3	SALQQAWFFFEFELMVKSMVHHLYFNDKLEARKSRFPFERFMDIAALVSTIASDIVSRFQK
HC5	-----
HC2A	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
KIAA	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
rat	-----
HC4	IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
HC1	ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLQCQYKFDL
HC3	DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYQVSSKLYSLPNPSVLVSLRLDFL
HC5	-----
HC2A	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF
KIAA	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF
rat	-----
HC4	QTICNHEHYIPLNLPM-----AFAKPKLQR-----VQDSNL----EYSLSDEY
HC1	QEVQCQHEHFIPCLPIRSANIPDLTPSES-----TQELHASDMPESVSTNEF
HC3	RIICSHHYVTLNLPCSLTTPASPSPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF
HC5	-----MNADTAPTSPCPSIS---SQNSSSCSSSQDQKIASMFDRTSRVPA
	Cadherin EC motif
HC2A	CRNHFLVGILLREVG TALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA	CRNHFLVGILLREVG TALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat	-----
HC4	CKHHFLVGILLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQ
HC1	CRKHFLIGILLREVG FALQEDQD----VRHLALAVLKNLMKHSFDDRYREPRKQAQIAS
HC3	RQQHYLAGIVLTELAVILDPDAEGLFGLHKKVINMVHNLLSSHSDPRYSDPQIKARVAM
HC5	SSTS-SPGILFTELAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAA
HC2A	LYLPLFGLLIENVQRINVRDVSPPFVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
KIAA	LYLPLFGLLIENVQRINVRDVSPPFVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
rat	-----
HC4	LYLPLFVGLLLENIQRLAGRDTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS
HC1	LYMPYGMLLDNMPRIYKLDLYPFTVNTSNQGSRDDLTNGGFQSQTAIKHANSVDTSFS
HC3	LYLPLIGIIMETVPQLYDFTETHNQRGRPICIAATDDYESE-----SG--SMIS
HC5	LYLPLVGII LDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT

FIG. 3A (2 of 5)

HHC2A	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS
KIAA	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS
rat	-----
HC4	TDKDTAYGSFQNG-----HGIKREDSRGSLIP-EGATGFPDQNGTGEN-----TRQS
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL
HC3	QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----
HC5	QNALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----
HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKMSDDALFTYWN-KASTSELMDFFTISEVCL
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKMSDDALFTYWN-KASTSELMDFFTISEVCL
rat	-----
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLLTYWN-KVSPQELINILILLEVCL
HC1	ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
HC3	-----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQNLRLDLLLYLCV
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRLDLLFICV
HC2A	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLFVSRNRTGMM
KIAA	HQFQYMGKRYIAR-----TGMM
rat	-----
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALNRNSGVM
HC1	QNFERYLGKRNIIRKIAAAF--KFVQSTQNNGLKGSNPSCQTSGLLAQWMHSTSRHEGHK
HC3	SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV
HC5	LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEARGEMM
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
rat	-----
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS
HC1	QHRSQTLPIIRGK---NALSNPKL---LQMLDNTMTSNEIDIVHHVDTEANIATEGC
HC3	RRSRGQLERSPSGSFAGSQENLRWRKDMTHWRQNTKLDKSRAEIEHEALIDGNLATEAN
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH
HC2A	LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
rat	-----KLSRGHSPLMKKVFDVYLCFLQKHQSEMALKNVFTALRSLIY
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
HC1	LTILDVLSLFTQTHQRQLQCCDCQNSLMKRGFDTYMLFFQVQNQSATALKHVFASLRFLVC
HC3	LIILDTLEIVVQTVS--VTES--KESILGGVLKVLLHSMACNQSAVYLQHCFAQTRALVS
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSINCDQSTTYLTHCFATLRALIA
HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
HC4	KFPSAFFKGRVNMCAAFCEYVLKCCTSKISSRNEASALLYLLMRNNFEYTKRKTFLRTH
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3	KFPELLFEEETEQCADLCLRLLRHCSSSIGTIRSHPSASLYLLMRQNFEIGN--NFARVK
HC5	KFGDLLFEEVEEQCFDLCHQVLHHCSSMDVTRSQCACATLYLLMRFSFGATS--NFARVK
HC2A	LQVIISVSQLIADVVGIGETRQQSLSIINNCA NSDRLIKHTSFSSDVKDLTKRIRTVLM
KIAA	LQVIISVSQLIADVVGIGETRQQSLSIINNCA NSDRLIKHTSFSSDVKDLTKRIRTVLM
rat	LQVIISLSQLIADVVGIGETRQQSLSIINNCA NSDRLIKHTSFSSDVKDLTKRIRTVLM
HC4	LQIIIAVSQLIADVALSGGSRFQESLFIINNFA NSDRPMLARAFPAEVKDLTKRIRTVLM
HC1	LQLIKAVSQLIAD-AGIGGSRFQHS LAITNNFANGDKQMKN SNFPAEVKDLTKRIRTVLM
HC3	MQVPMSSLSSLVGTSQNFNEEFLRRSLKTI LTYAEEDLELRETTFPDQVQDLVFNLMHILS
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRITILAYSEEDTAMQMTFPFPTQVEELLCNLNSILY

FIG. 3A (3 of 5)

Transmembrane

HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGDLSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGDLSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGDLSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD SMAKIHVKNDFSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHT
HC3	DTVKMKEHQEDPEMLIDL MYRIAKGYQTSPDLRLTWLQNMAGKHSERSNHAEEAQCCLVHS
HC5	DTVKMREFQEDPEMLMDL MYRIAKSYQASPDRLRLTWLQNMAEKHTKKKCYTEAAMCLVHA

SH3

HC2A	TALVAEYLTRKGV-----	-----FRQGCTAFRVITPN
KIAA	TALVAEYLTRKEA-----	-----VQWEPPLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat	TALVAEYLTRKEAD-----	-----LALQREPPVPFYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEFLHRKKL-----	-----FPNGCSAFKKITPN
HC1	AALIAEYLRKRGYWKVEIK-----	-----TASLLSEDTHPCDNSNLLTTPSGGSMFSGWPAFLSITPN
HC3	AALVAEYLSMLED-----	-----RKYLPVGCVTTFQNISSN
HC5	AALVAEYLSMLED-----	-----HSYLPVGSVSFQNISSN

ITAM

HC2A	IDEEASMMEDVGMQD-----	-----VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI
KIAA	IDEEASMMEDVGMQD-----	-----VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI
rat	IDEEASMMEDVGMQD-----	-----VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4	IDEEGAMKEDAGMMD-----	-----VHYSEEVLLELLEQCVNGLWKAERYEITSEISKILGPI
HC1	IKEEGAAKEDSGMHD-----	-----TPYNENILVEQLYMCGEFLWKSERYELIADVKNPIIAV
HC3	VLEESAVSDDVSPDEEGICSGKYFTESGLVGLLEQAAASF SMAGMYEAVNEVYKVLPIPI	
HC5	VLEESVVSSEDTLSPDEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVLPIPI	

ITAM ITAM

ITAM

ITAM

HC2A	YEKRRD-----			
KIAA	YEKRRD FERLAHL YDTLHRAYSKVTEVMHSGRLLGT YFRV AFFGQAAQYQFTDSETDVE			
rat	SMKSGGTLETTHLYDTLHRAYSKVTEVITR-----			A-----AGSWDLLPGGLFGQ
HC4	YENRREFENLTQVYRTIHGAYTKILEVMHTKKRLG-----			TFFRVAFYFGQ
HC1	FEKQRDFKKLSDIYYDIHRSYLVKVAEVDVNSEKRLFG-----			RYRVAFYFGQ
HC3	HEANRDAKKLSTIHGKLQEAFSKIVHQSTGWERMFG-----			TYFRVGFYFG-
HC5	LEAHREFRKLTLTHSKLQRAFDIVNKH--KRMFG-----			TYFRVGFYFG-

ITAM

ITAM

HC2A	-FFEDEDGKBYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA
KIAA	GFFEDEDGKBYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA
rat	GFFEDEDGKBYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA
HC4	SFFEEDDGKBYIYKEPKLTGLSEISRLRLVKLYGEKFGTENVKIIQDSDKVNAKELDPKYA
HC1	GFFEEEEGKBYIYKEPKLTGLSEISQRLLKLYADKFGADNVKIIQDSNKNVNPKDLDPKYA
HC3	TKFGDLDEQBFVYKEPAITKLAEISRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKA
HC5	SKFGDLDEQBFVYKEPAITKLPEISRLEAFYGCFCGAEFVEVIKDSNPVDKCKLDPNKA

ITAM

HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
rat	YIQVTHVIPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
HC4	HIQVTVVKPYFDDKELTERKTEFERNHNISRFVFEAPYTLGSKKQGCIEEQCKRRTILTT
HC1	YIQVTVVTPFFEEKEIEDRKTD FEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILTT
HC3	YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMCTPFTLDGRAHGELEQFKRKTIILTT
HC5	YIQITYVEPYFDEYEMKDRVITYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLT

FIG. 3A (4 of 5)

	Coiled-Coil 1
HC2A	IHCFFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
KIAA	IHCFFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
rat	IHCFFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLQGSV
HC4	SNSFPYVKKRIPINCEQQINLKPIDGATDEIKDKTAELQKLCSTDVDMIQLQLKLQGSV
HC1	SHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV
HC3	SHAFPIKTRVNVTHKEEIIILTPIEVAIEDMQKKTQELAFATHQDPADPKMLQMVLCQSV
HC5	MHAFPIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINQEPDAKMLQMVLCQSV

	Coiled-Coil 2
HC2A	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
rat	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
HC4	SVQVNAGPLAYARAFLLDSQASKYPKKVSELKDMFRKFIQACSI ALELNERLIKEDQVE
HC1	SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLE
HC3	GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKNKSLIGPVQKE
HC5	GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE

	Coiled-Coil 2
HC2A	YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPSTMTVHGMTSS
KIAA	YQEEMKANYREMAKELSEIMHEQLG-----
rat	YQEEMKANYREIRKELSDIIVERICPGEDKRATKFP AHLQRHQRDTNKHSGSRVDQFILS
HC4	YHEGLKSNFRDMVKELSDIIEHQILQEDTMHSPWMSNTLHVFC AISGTSSDRGYGSPRYA
HC1	YQEELRSHYKDMSELSTVMNEQITGRDDLK---RGVDQTCTRVISKATPALPTVISISS
HC3	YQRELG---KLSS-----P-----
HC5	YQELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS--

	PBM
HC2A	SSVV-----
KIAA	-----
rat	CVTLPHPEPHVGTCTFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWTVIFNSRFYRSWKG
HC4	EV-----
HC1	SAEV-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	-----
rat	VHIF
HC4	-----
HC1	-----
HC3	-----
HC5	-----

FIG. 3A (5 of 5)

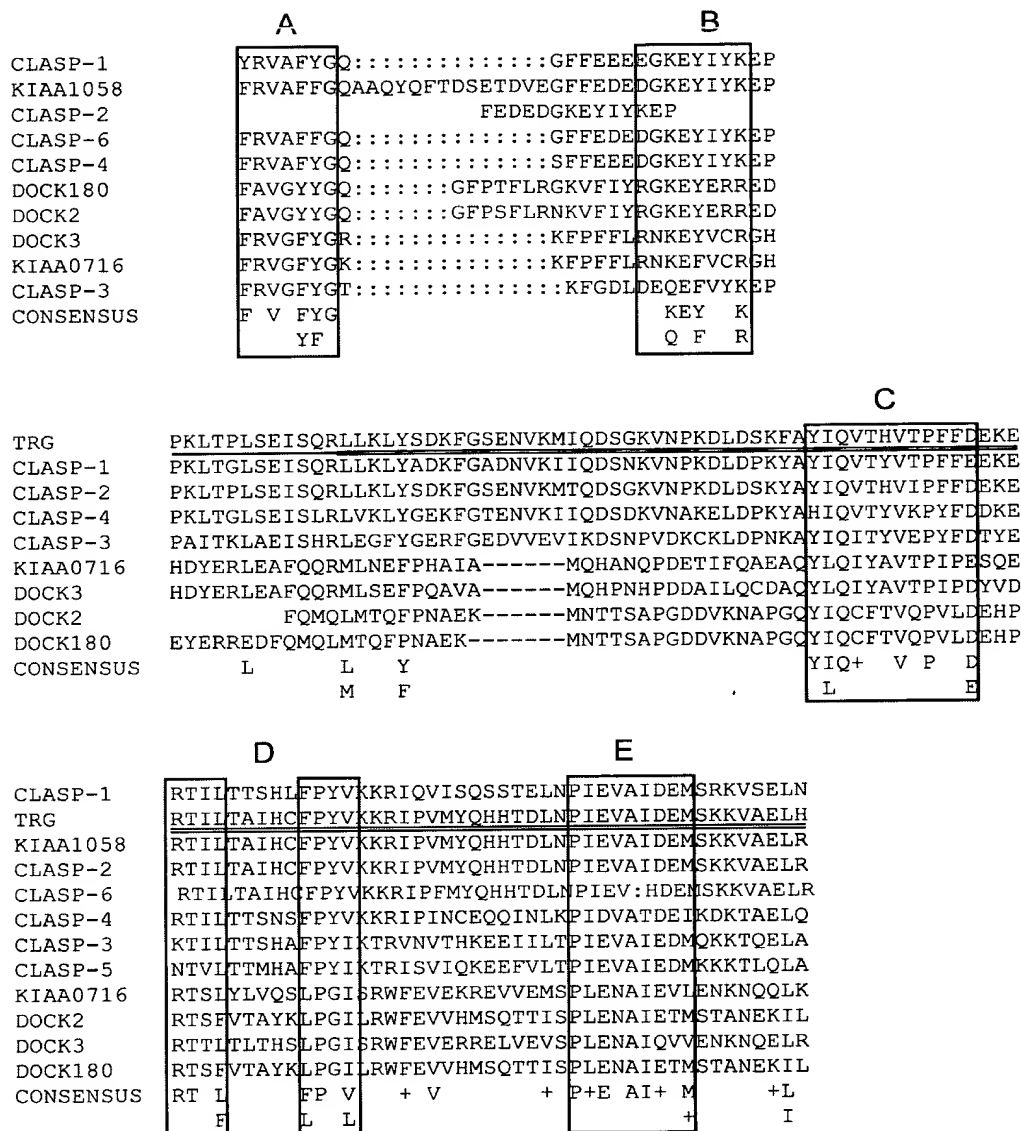


FIG. 3B (1 of 2)

[illegible]

FIG. 3B (2 of 2)

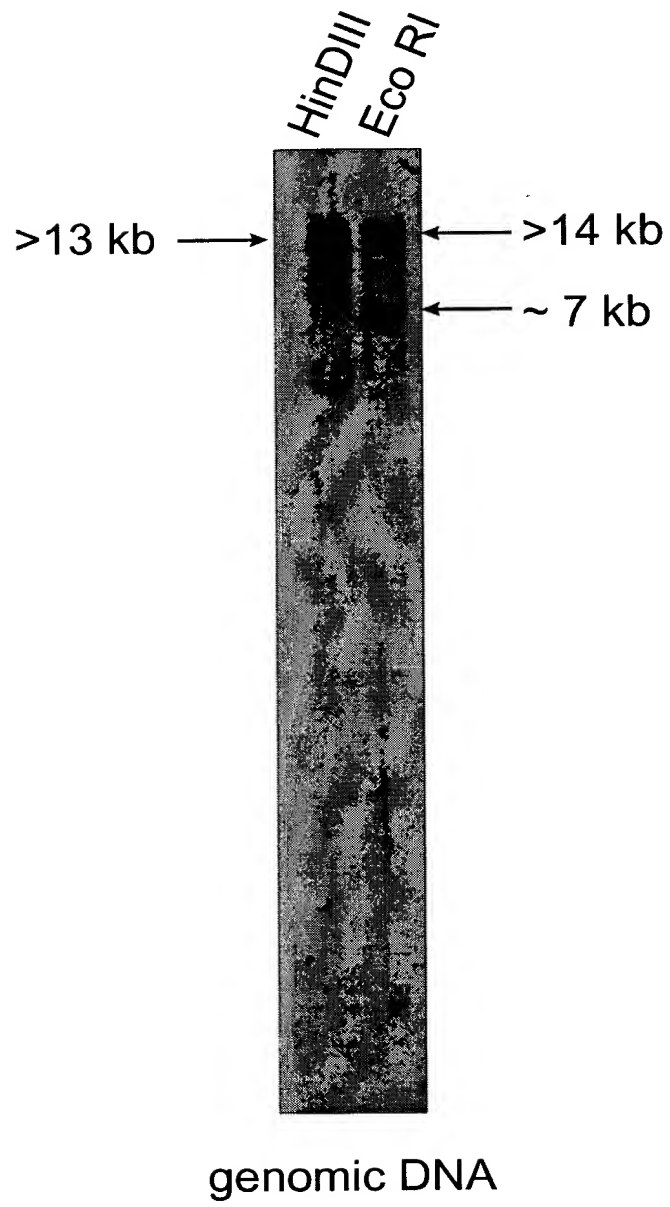


FIG. 4

-12 -1
GACGCGAGGACC

1/1	31/11
ATG GCT GCC TCC GAG CGC CGC GCC TTC GCG	CAC AAG ATC AAC AGG ACG GTG GCC GCA GAG
Met ala ala ser glu arg arg ala phe ala	his lys ile asn arg thr val ala ala glu
61/21	91/31
GTG CGG AAG CAG GTG TCC CGG GAA CGC AGT	GGC TCC CCC CAC TCC AGC AGG CGC TGC AGC
val arg lys gln val ser arg glu arg ser	gly ser pro his ser ser arg arg cys ser
121/41	151/51
AGC TCC CTG GGG GTC CCA CTG ACT GAA GTT	GTC GAG CCC CTG GAC TTT GAG GAT GTA CTT
ser ser leu gly val pro leu thr glu val	val glu pro leu asp phe glu asp val leu
181/61	211/71
CTG AGC CGG CCA CCA GAT GCT GAG CCC GGG	CCC CTC AGG GAC CTG GTA GAA TTC CCA GCT
leu ser arg pro pro asp ala glu pro gly	pro leu arg asp leu val glu phe pro ala
241/81	271/91
GAT GAC TTG GAG CTG CTG CTG CAG CCC CGG	GAA TGC CGG ACC ACG GAG CCC GGG ATC CCC
asp asp leu glu leu leu leu gln pro arg	glu cys arg thr thr glu pro gly ile pro
301/101	331/111
AAG GAT GAA AAA CTG GAT GCC CAG GTG AGG	GCC GCG GTG GAG ATG TAT ATT GAG GAC TGG
lys asp glu lys leu asp ala gln val arg	ala ala val glu met tyr ile glu asp trp
361/121	391/131
GTC ATT GTC CAC AGA AGG TAT CAG TAC CTG	AGT GCA GCA TAC AGC CCC GTC ACC ACA GAC
val ile val his arg arg tyr gln tyr leu	ser ala ala tyr ser pro val thr thr asp
421/141	451/151
ACA CAG CGG GAG CGA CAG AAG GGC CTC CCC	CGC CAG GTC TTT GAG CAG GAT GCT TCT GGA
thr gln arg glu arg gln lys gly leu pro	arg gln val phe glu gln asp ala ser gly
481/161	511/171
GAC GAG AGG TCC GGC CCT GAG GAC TCG AAT	GAC TCC CGG CGT GGC TCG GGC TCC CCG GAA
asp glu arg ser gly pro glu asp ser asn	asp ser arg arg gly ser gly ser pro glu
541/181	571/191
GAC ACC CCT CGA AGC AGT GGT GCC TCT AGC	ATC TTC GAC CTG AGG AAC CTG GCA GCT GAC
asp thr pro arg ser ser gly ala ser ser	ile phe asp leu arg asn leu ala ala asp
601/201	631/211
TCA TTG CTG CCC TCT CTG CTA GAG CGG GCG	GCC CCA GAA GAT GTG GAC CGG CGC AAT GAA
ser leu leu pro ser leu leu glu arg ala	ala pro glu asp val asp arg arg asn glu
661/221	691/231
ACC CTT CGA CGG CAG CAC CGG CCC CCG GCC	CTG CTC ACC CTC TAC CCG GCA CCT GAC GAG
thr leu arg arg gln his arg pro pro ala	leu leu thr leu tyr pro ala pro asp glu
721/241	751/251
GAT GAA GCC GTG GAA CGC TGT AGC CGC CCA	GAG CCA CCC CGC GAG CAC TTT GGA CAA AGG
asp glu ala val glu arg cys ser arg pro	glu pro pro arg glu his phe gly gln arg
781/261	811/271
ATC TTG GTC AAG TGT CTG TCG CTC AAG TTC	GAG ATT GAA ATT GAG CCC ATC TTT GGG ATC
ile leu val lys cys leu ser leu lys phe	glu ile glu ile glu pro ile phe gly ile
841/281	871/291
TTG GCT CTG TAT GAT GTG CGG GAG AAA AAG	AAG ATC TCG GAG AAC TTC TAC TTC GAC CTG
leu ala leu tyr asp val arg glu lys lys	lys ile ser glu asn phe tyr phe asp leu
901/301	931/311
AAC TCG GAC TCC ATG AAG GGG CTG CTT CGG	GCT CAT GGC ACC CAC CCT GCC ATC TCC ACC
asn ser asp ser met lys gly leu leu arg	ala his gly thr his pro ala ile ser thr
961/321	991/331
CTG GCC CGC TCT GCC ATC TTC TCT GTG ACC	TAC CCC TCA CCT GAC ATC TTC CTG GTC ATC
leu ala arg ser ala ile phe ser val thr	tyr pro ser pro asp ile phe leu val ile
1021/341	1051/351
AAG TTG GAG AAG GTG CTT CAG CAA GGG GAC	ATC AGT GAG TGC TGT GAG CCT TAC ATG GTG
lys leu glu lys val leu gln gln gly asp	ile ser glu cys cys glu pro tyr met val
1081/361	1111/371
TTG AAA GAA GTG GAC ACA GCC AAG AAC AAA	GAG AAG CTA GAG AAG CTG CGC CTG GCG GCC
leu lys glu val asp thr ala lys asn lys	glu lys leu glu lys leu arg leu ala ala

09736966-101201

FIG. 5A (1 of 6)

1141/381	GAG CAG TTC TGC ACC CGC CTG GGC CGC TAC	1171/391	CGC ATG CCC TTC GCC TGG ACG GCC GTG CAC
1201/401	glu gln phe cys thr arg leu gly arg tyr	1231/411	arg met pro phe ala trp thr ala val his
1261/421	TTG GCC AAC ATC GTG AGC AGC GCT GGG CAG	1291/431	CTG GAC CGG GAC TCT GAC TCG GAG GGC GAG
1321/441	leu ala asn ile val ser ser ala gly gln	1351/451	leu asp arg asp ser asp ser glu gly glu
1381/461	CGC CGG CCA GCC TGG ACA GAC CGC CGC CGT	1411/471	CGG GGG CCC CAG GAC CGG GCG AGT AGT GGG
1441/481	arg arg pro ala trp thr asp arg arg arg	1471/491	arg gly pro gln asp arg ala ser ser gly
1501/501	GAC GAC GCC TGC AGC TTC TCT GGC TTC CGT	1531/511	CCA GCC ACG CTA ACT GTC ACA AAC TTC TTT
1561/521	asp asp ala cys ser phe ser gly phe arg	1591/531	pro ala thr leu thr val thr asn phe phe
1621/541	AAG CAG GAG GCT GAG CGA CTC AGT GAC GAG	1651/551	GAC CTC TTC AAG TTC CTG GCT GAC ATG AGG
1681/561	lys gln glu ala glu arg leu ser asp glu	1711/571	asp leu phe lys phe leu ala asp met arg
1741/581	CGC CCG TCG TCC CTG CTG CGG CGA CTA CGT	1771/591	CCT GTG ACT GCC CAG CTC AAG ATC GAC ATT
1801/601	arg pro ser ser leu leu arg arg leu arg	1831/611	pro val thr ala gln leu lys ile asp ile
1861/621	TCT CCG GCT CCT GAA AAT CCC CAC TTC TGC	1891/631	CTC TCC CCT GAG CTG CTT CAT ATC AAG CCC
1921/641	ser pro ala pro glu asn pro his phe cys	1951/651	leu ser pro glu leu leu his ile lys pro
1981/661	TAC CCG GAC CCC AGG GGC CGG CCC ACC AAG	2011/671	GAG ATT CTG GAG TTC CCC GCC CGC GAA GTC
2041/681	tyr pro asp pro arg gly arg pro thr lys	2071/691	glu ile leu glu phe pro ala arg glu val
2101/701	TAT GCC CCC CAT ACC AGC TAC AGG AAC CTG	2131/711	CTG TAC GTG TAC CCG CAC AGC CTC AAC TTC
2161/721	tyr ala pro his thr ser tyr arg asn leu	2191/731	leu tyr val tyr pro his ser leu asn phe
2221/741	AGC AGC CGC CAG GGC TCC GTG CGC AAC CTT	2251/751	GCT GTG CGA GTG CAG TAC ATG ACA GGC GAG
	ser ser arg gln gly ser val arg asn leu		ala val arg val gln tyr met thr gly glu
	GAC CCC AGC CAG GCT CTG CCG GTC ATC TTT		1771/591
	asp pro ser gln ala leu pro val ile phe		GGC AAG TCC AGC TGC AGT GAA TTT ACC CGC
	1801/601		gly lys ser ser cys ser glu phe thr arg
	GAG GCC TTC ACA CCG GTG GTC TAC CAT AAC		1831/611
	glu ala phe thr pro val val tyr his asn		AAG TCC CCC GAG TTC TAC GAG GAG TTC AAG
	1861/621		lys ser pro glu phe tyr glu glu phe lys
	CTG CAT CTT CCA GCC TGC GTG ACA GAG AAC		1891/631
	leu his leu pro ala cys val thr glu asn		CAT CAC CTG CTG TTC ACC TTC TAC CAT GTC
	1921/641		his his leu leu phe thr phe tyr his val
	AGC TGC CAG CCC CGG CCG GGC ACT GCC CTG		1951/651
	ser cys gln pro arg pro gly thr ala leu		GAG ACA CCC GTG GGC TTT ACT TGG ATC CCA
	1981/661		glu thr pro val gly phe thr trp ile pro
	CTG CTG CAG CAC GGG CGC CTG AGG ACC GGC		2011/671
	leu leu gln his gly arg leu arg thr gly		CCC TTC TGT CTC CCA GTG TCT GTG GAC CAG
	2041/681		pro phe cys leu pro val ser val asp gln
	CCG CCG CCC AGC TAT TCC GTG CTC ACA CCC		2071/691
	pro pro pro ser tyr ser val leu thr pro		GAT GTG GCG CTT CCG GGC ATG CGC TGG GTG
	2101/701		asp val ala leu pro gly met arg trp val
	GAC GGT CAC AAG GGC GTG TTC AGT GTG GAG		2131/711
	asp gly his lys gly val phe ser val glu		CTC ACA GCC GTG TCC TCT GTG CAC CCC CAG
	2161/721		leu thr ala val ser ser val his pro gln
	GAC CCC TAC CTG GAC AAA TTC TTC ACC CTG		2191/731
	asp pro tyr leu asp lys phe phe thr leu		GTG CAC GTC CTG GAG GAG GGA GCC TTC CCA
	2221/741		val his val leu glu glu gly ala phe pro
	TTC CGG CTC AAG GAC ACT GTG CTG AGC GAG		2251/751
	phe arg leu lys asp thr val leu ser glu		GGC AAC GTG GAG CAG GAG CTG CGG GCC AGT
			gly asn val glu gln glu leu arg ala ser

FIG. 5A (2 of 6)

2281/761	CTT GCA GCA CTG CGC CTG GCC AGC CCC GAA	2311/771	CCC CTT GTG GCC TTC TCC CAC CAC GTG CTG
leu ala ala leu arg leu ala ser pro glu	pro leu val ala phe ser his his val leu		
2341/781	GAC AAG CTC GTG CGT CTG GTC ATC AGG CCC	2371/791	CCG ATC ATC AGT GGC CAG ATT GTG AAC CTG
asp lys leu val arg leu val ile arg pro	pro ile ile ser gly gln ile val asn leu		
2401/801	GGC CGT GGA GCC TTT GAA GCA ATG GCC CAT	2431/811	GTA GTC AGC CTT GTT CAC CGG AGC CTG GAG
gly arg gly ala phe glu ala met ala his	val val ser leu val his arg ser leu glu		
2461/821	GCA GCC CAG GAT GCC CGC GGT CAC TGC CCA	2491/831	CAG CTG GCT GCC TAC GTC CAC TAC GCC TTT
ala ala gln asp ala arg gly his cys pro	gln leu ala ala tyr val his tyr ala phe		
2521/841	CGC CTT CCT GGC ACT GAG CCC AGC CTC CCG	2551/851	GAT GGG GCC CCT CCA GTG ACA GTG CAG GCT
arg leu pro gly thr glu pro ser leu pro	asp gly ala pro pro val thr val gln ala		
2581/861	GCC ACA CTG GCC CGT GGC TCT GGT CGC CCC	2611/871	GCA AGC CTC TAC CTG GCG CGT TCC AAG AGC
ala thr leu ala arg gly ser gly arg pro	ala ser leu tyr leu ala arg ser lys ser		
2641/881	ATC AGC AGC AGC AAC CCT GAC CTC GCC GTG	2671/891	GCC CCT GGC TCT GTG GAT GAC GAG GTT TCC
ile ser ser ser asn pro asp leu ala val	ala pro gly ser val asp asp glu val ser		
2701/901	CGC ATC CTG GCC AGC AAG CTG CTT CAC GAG	2731/911	GAG CTG GCT CTG CAG TGG GTG GTC AGC AGC
arg ile leu ala ser lys leu leu his glu	glu leu ala leu gln trp val val ser ser		
2761/921	AGT GCC GTA CGC GAG GCC ATC CTC CAG CAC	2791/931	GCC TGG TTC TTC TTC CAG CTC ATG GTG AAG
ser ala val arg glu ala ile leu gln his	ala trp phe phe phe gln leu met val lys		
2821/941	AGT ATG GCG CTG CAC CTG CTG CTT GGC CAG	2851/951	CGA CTA GAC ACA CCC CGC AAG CTG CGC TTC
ser met ala leu his leu leu leu gly gln	arg leu asp thr pro arg lys leu arg phe		
2881/961	CCC GGA CGC TTC CTG GAC GAC ATC ACT GCC	2911/971	TTG GTG GGC TCT GTG GGC CTG GAG GTC ATC
pro gly arg phe leu asp asp ile thr ala	leu val gly ser val gly leu glu val ile		
2941/981	ACC CGT GTC CAC AAG GAT GTG GAG CTG GCC	2971/991	GAG CAC CTC AAC GCC AGC CTG GCT TTC TTC
thr arg val his lys asp val glu leu ala	glu his leu asn ala ser leu ala phe phe		
3001/1001	CTC AGT GAC CTT CTG TCC CTG GTG GAC CGG	3031/1011	GGC TTT GTC TTC AGC CTG GTC CGG GCC CAC
leu ser asp leu leu ser leu val asp arg	gly phe val phe ser leu val arg ala his		
3061/1021	TAC AAG CAG GTG GCC ACG CGG CTC CAG TCG	3091/1031	TCC CCT AAT CCA GCA GCC CTG CTG ACC CTG
tyr lys gln val ala thr arg leu gln ser	ser pro asn pro ala ala leu leu thr leu		
3121/1041	CGC ATG GAA TTC ACC CGC ATC CTG TGC AGC	3151/1051	CAC GAG CAC TAC GTG ACC CTC AAC CTC CCC
arg met glu phe thr arg ile leu cys ser	his glu his tyr val thr leu asn leu pro		
3181/1061	TGC TGC CCC CTG TCA CCT CCA GCC TCG CCC	3211/1071	TCC CCC TCT GTG TCC TCC ACC ACC TCC CAG
cys cys pro leu ser pro pro ala ser pro	ser pro ser val ser ser thr thr ser gln		
3241/1081	AGC TCC ACC TTC TCC AGC CAA GCC CCG GAC	3271/1091	CCC AAG GTG ACC AGC ATG TTC GAA CTG AGT
ser ser thr phe ser ser gln ala pro asp	pro lys val thr ser met phe glu leu ser		
3301/1101	GGA CCA TTC CGG CAG CAG CAC TTC CTA GCT	3331/1111	GGG CTC CTG CTG ACG GAG CTG GCA CTG GCC
gly pro phe arg gln gln his phe leu ala	gly leu leu leu thr glu leu ala leu ala		
3361/1121	CTC GAA CCT GAG GCT GAA GGG GCA TTC CTG	3391/1131	TTG CAC AAG AAG GCC ATC AGT GCT GTG CAC
leu glu pro glu ala glu gly ala phe leu	leu his lys lys ala ile ser ala val his		
3421/1141	AGC CTG CTA TGT GGC CAT GAC ACT GAC CCC	3451/1151	CGC TAC GCC GAG GCC ACT GTG AAG GCT CGT
ser leu leu cys gly his asp thr asp pro	arg tyr ala glu ala thr val lys ala arg		
3481/1161	GTG GCC GAG CTG TAC CTG CCA CTG CTT TCG	3511/1171	ATT GCA CGG GAT ACC TTG CCA CGG CTG CAT
val ala glu leu tyr leu pro leu leu ser	ile ala arg asp thr leu pro arg leu his		

FIG. 5A (3 of 6)

3541/1181	GAC TTT GCT GAG GGC CCA GGT CAG CGG TCA	3571/1191	AGA CTG GCC TCA ATG CTT GAC TCA GAC ACA
asp phe ala glu gly pro gly gln arg ser		arg leu ala ser met leu asp ser asp thr	
3601/1201	GAA GGC GAA GGG GAC ATT GCG GGT ACC ATC	3631/1211	AAC CCC TCT GTG GCC ATG GCC ATT GCT GGT
glu gly glu gly asp ile ala gly thr ile		asn pro ser val ala met ala ile ala gly	
3661/1221	GGC CCC CTA GCC CCT GGC TCC CGG GCC AGC	3691/1231	ATC TCC CAG GGG CCA CCA ACG GCT TCT CGC
gly pro leu ala pro gly ser arg ala ser		ile ser gln gly pro pro thr ala ser arg	
3721/1241	GCA GGC TGT GCC CTC TCT GCT GAG TCA AGC	3751/1251	CGG ACC TTG CTG GCG TGT GTG CTG TGG GTG
ala gly cys ala leu ser ala glu ser ser		arg thr leu leu ala cys val leu trp val	
3781/1261	CTG AAA AAC ACC GAG CCG GCG CTC CTG CAG	3811/1271	CGC TGG GCC ACT GAC CTG ACA CTC CCC CAG
leu lys asn thr glu pro ala leu leu gln		arg trp ala thr asp leu thr leu pro gln	
3841/1281	CTG GGA CGT CTG TTG GAC TTG CTG TAC CTT	3871/1291	TGC CTG GCT GCC TTT GAG TAC AAG GGG AAA
leu gly arg leu leu asp leu leu tyr leu		cys leu ala ala phe glu tyr lys gly lys	
3901/1301	AAG GCC TTT GAA CGC ATC AAC AGC CTC ACA	3931/1311	TTC AAA AAA TCT CTG GAT ATG AAG GCG CGG
lys ala phe glu arg ile asn ser leu thr		phe lys lys ser leu asp met lys ala arg	
3961/1321	CTA GAG GAA GCC ATT CTG GGT ACC ATC GGA	3991/1331	GCT CGA CAA GAA ATG GTT CGG CGA AGT CGT
leu glu glu ala ile leu gly thr ile gly		ala arg gln glu met val arg arg ser arg	
4021/1341	GAG AGG AGC CCG TTT GGG AAT CCA GAG AAC	4051/1351	GTG CGC TGG CGG AAG AGC GTC ACA CAC TGG
glu arg ser pro phe gly asn pro glu asn		val arg trp arg lys ser val thr his trp	
4081/1361	AAG CAA ACC TCA GAC CGC GTG GAC AAG ACC	4111/1371	AAG GAT GAA ATG GAA CAC GAG GCC TTG GTG
lys gln thr ser asp arg val asp lys thr		lys asp glu met glu his glu ala leu val	
4141/1381	GAA GGG AAC CTG GCA ACC GAG GCA AGC CTA	4171/1391	GTG GTT CTG GAC ACA CTG GAG ATC ATC GTG
glu gly asn leu ala thr glu ala ser leu		val val leu asp thr leu glu ile ile val	
4201/1401	CAG ACG GTG ATG CTT TCA GAA GCC CGG GAG	4231/1411	AGC GTC TTG GGG GCA GTG CTG AAG GTT GTG
gln thr val met leu ser glu ala arg glu		ser val leu gly ala val leu lys val val	
4261/1421	CTG TAC AGC CTG GGC AGT GCC CAG AGT GCC	4291/1431	CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG
leu tyr ser leu gly ser ala gln ser ala		leu phe leu gln his gly leu ala thr gln	
4321/1441	AGG GCC CTT GTG TCC AAG TTC CCG GAG CTG	4351/1451	CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC
arg ala leu val ser lys phe pro glu leu		leu phe glu glu asp thr glu leu cys ala	
4381/1461	GAC CTG TGC CTG AGG CTC CTA CGA CAC TGT	4411/1471	GGC AGC CGC ATC AGC ACC ATC CGC ACG CAC
asp leu cys leu arg leu leu arg his cys		gly ser arg ile ser thr ile arg thr his	
4441/1481	GCC AGC GCC TCG CTG TAC CTG CTC ATG CGA	4471/1491	CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC
ala ser ala ser leu tyr leu leu met arg		gln asn phe glu ile gly his asn phe ala	
4501/1501	CGT GTG AAG ATG CAG GTC ACC ATG TCT CTC	4531/1511	TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC
arg val lys met gln val thr met ser leu		ser ser leu val gly thr thr gln asn phe	
4561/1521	AGT GAA GAG CAC CTG CGA CGT TCA CTC AAA	4591/1531	ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG
ser glu glu his leu arg arg ser leu lys		thr ile leu thr tyr ala glu glu asp met	
4621/1541	GGG CTG CGG GAC AGC ACC TTC GCA GAG CAG	4651/1551	GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG
gly leu arg asp ser thr phe ala glu gln		val gln asp leu met phe asn leu his met	
4681/1561	ATC CTG ACG GAC ACG GTG AAG ATG AAG GAA	4711/1571	CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC
ile leu thr asp thr val lys met lys glu		his gln glu asp pro glu met leu ile asp	

FIG. 5A (4 of 6)

4741/1581	CTC ATG TAC AGA ATT GCC CGG GGC TAC CAG	4771/1591	GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG
leu met tyr arg ile ala arg gly tyr gln		gly ser pro asp leu arg leu thr trp leu	
4801/1601	CAG AAC ATG GCC GGG AAG CAC GCG GAG CTG	4831/1611	GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG
gln asn met ala gly lys his ala glu leu		gly asn his ala glu ala ala gln cys met	
4861/1621	GTG CAC GCG GCC GCC CTC GTG GCT GAG TAC	4891/1631	CTC GCC CTG CTC GAG GAC CAG CGC CAC CTG
val his ala ala ala leu val ala glu tyr		leu ala leu leu glu asp gln arg his leu	
4921/1641	CCC GTG GGC TGC GTT TCC TTC CAG AAC ATC	4951/1651	TCA TCC AAC GTG CTA GAG GAG TCC GCC ATC
pro val gly cys val ser phe gln asn ile		ser ser asn val leu glu glu ser ala ile	
4981/1661	TCC GAC GAC ATC CTG TCG CCC GAC GAG GAG	5011/1671	GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG
ser asp asp ile leu ser pro asp glu glu		gly phe cys ser gly lys his phe thr glu	
5041/1681	CTG GGG CTG GTA GGG TTG CTG GAA CAG GCA	5071/1691	GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC
leu gly leu val gly leu leu glu gln ala		ala gly tyr phe thr met gly gly leu tyr	
5101/1701	GAG GCG GTG AAT GAG GTC TAC AAG AAC CTC	5131/1711	ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC
glu ala val asn glu val tyr lys asn leu		ile pro ile leu glu ala his arg asp tyr	
5161/1721	AAG AAG CTG GCC GCG GTG CAC GGC AAA CTG	5191/1731	CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG
lys lys leu ala ala val his gly lys leu		gln glu ala phe thr lys ile met his gln	
5221/1741	AGT TCC GGC TGG GAG CGC GTG TTC GGG ACG	5251/1751	TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC
ser ser gly trp glu arg val phe gly thr		tyr phe arg val gly phe tyr gly ala his	
5281/1761	TTC GGT GAC CTG GAT GAG CAG GAG TTT GTG	5311/1771	TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA
phe gly asp leu asp glu gln glu phe val		tyr lys glu pro ser ile thr lys leu ala	
5341/1781	GAG ATC TCA CAC CGG CTG GAG GAG TTC TAC	5371/1791	ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG
glu ile ser his arg leu glu glu phe tyr		thr glu arg phe gly asp asp val val glu	
5401/1801	ATT ATC AAA GAC TCT TAC CCT GTG GAC AAG	5431/1811	TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC
ile ile lys asp ser tyr pro val asp lys		ser lys leu asp ser gln lys ala tyr ile	
5461/1821	CAG ATC ACG TAT GTG GAA CCG TAC TTT GAT	5491/1831	ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC
gln ile thr tyr val glu pro tyr phe asp		thr tyr glu leu lys asp arg val thr tyr	
5521/1841	TTT GAC CGC AAC TAT GGG CTT CGC ACA TTC	5551/1851	CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG
phe asp arg asn tyr gly leu arg thr phe		leu phe cys thr pro phe thr pro asp gly	
5581/1861	CGC GCA CAC GGG GAG CTG CCC GAG CAA CAC	5611/1871	AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC
arg ala his gly glu leu pro glu gln his		lys arg lys thr leu leu ser thr asp his	
5641/1881	GCC TTC CCC TAC ATC AAG ACT CGC ATC CGT	5671/1891	GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG
ala phe pro tyr ile lys thr arg ile arg		val cys his arg glu glu thr val leu thr	
5701/1901	CCA GTG GAG GTG GCC ATC GAG GAC ATG CAG	5731/1911	AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC
pro val glu val ala ile glu asp met gln		lys lys thr arg glu leu ala phe ala thr	
5761/1921	GAG CAG GAC CCA CCA GAT GCT AAG ATG CTA	5791/1931	CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC
glu gln asp pro pro asp ala lys met leu		gln met val leu gln gly ser val gly pro	
5821/1941	ACC GTG AAC CAG GGT CCC CTG GAG GTG GCC	5851/1951	CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC
thr val asn gln gly pro leu glu val ala		gln val phe leu ala glu ile pro glu asp	
5881/1961	CCC AAG CTC TTC CGG CAT CAC AAC AAA TTG	5911/1971	CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA
pro lys leu phe arg his his asn lys leu		arg leu cys phe lys asp phe cys lys lys	

FIG. 5A (5 of 6)

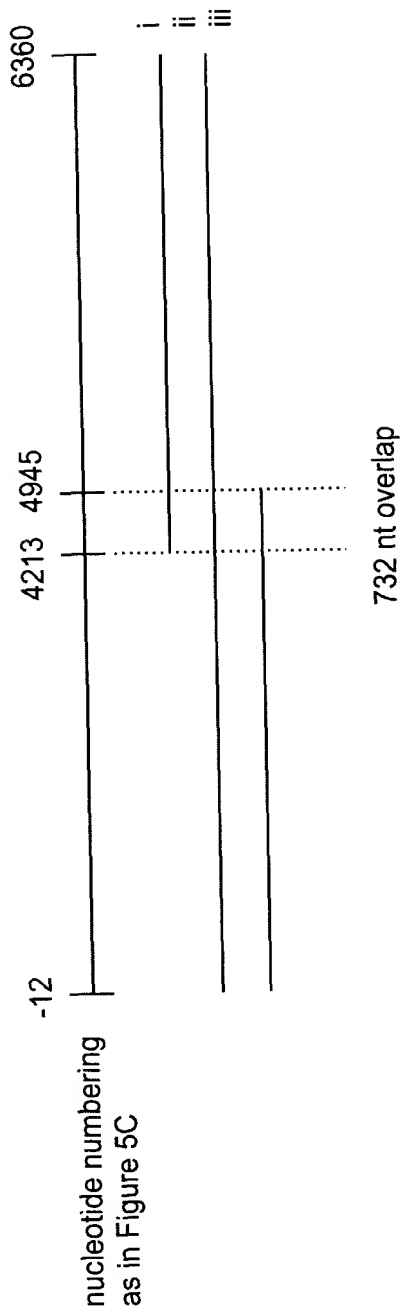
5941/1981	5971/1991
TGT GAG GAT GCG CTG CGG AAA AAT AAG GCC	CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC
cys glu asp ala leu arg lys asn lys ala	leu ile gly pro asp gln lys glu tyr his
6001/2001	6031/2011
CGT GAG CTG GAG CGC AAC TAC TGC CGC CTG	CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG
arg glu leu glu arg asn tyr cys arg leu	arg glu ala leu gln pro leu leu thr gln
6061/2021	6091/2031
CGC CTG CCC CAG CTG ATG GCA CCC ACC CCA	CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA
arg leu pro gln leu met ala pro thr pro	pro gly leu arg asn ser leu asn arg ala
6121/2041	6151/2051
AGT TTC CGA AAG GCA GAC CTC TGA GCC CAC	AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG
ser phe arg lys ala asp leu OPA	
6181/2061	6211/2071
CAC CCG GGC CTC AGC TGT CTG TGC TGC GAG	GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT
6241/2081	6271/2091
GGG GTG ACC ACA CTG TAC TTG GGG CTG GGC	CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA
6301/2101	6331/2111
CTG ATG CTT CCT CCC TTT TTT AAT TTA AAA	TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA

FIG. 5A (6 of 6)

[illegible]

These differences may be found separately or together in various combination in the difference human CLASP-7 isoforms

FIG. 5B (1 of 2)



Exon 63800 to 63920

GCGGGGCCGGGGCCCGGGCGGGCGGGCGGGACGCGAGGACCATGGCTGC
CTCCGAGCGCCGCGCTTCGCGCACAGATCAACAGGTAGTGTGGCCGCGGGG
 CCCCCTCCACCTCCC

Exon 72530 to 72670

CCAATGGCCCCCTCCCTATCTTTCCAGGACGGTGGCCGCAGAGGTGCGGAAG
CAGGTGTCCCGGAACGCAGTGGCTCCCCCACTCCAGCAGGCGCTGCAGCA
GCTCCCTGGGGGTAAAGTATTTGGGGGTCCGCCCCCA

Exon 73300 to 73530

TCACAGCCACTTTGCTCCAATCCAGGTCCCACTGACTGAAGTTGTGAGCCCC
TGGACTTTGAGGATGTACTTCTGAGCCGGCCACCAGATGCTGAGCCCGGGCC
CCTCAGGGACCTGGTAGAATCCCAGCTGATGACTTGGAGCTGCTGCTGCAG
CCCCGGGAATGCCGACCACGGAGCCCGGGATCCCCAAGGATGAGTGGGTTC
 AGCCCCACGCCCTCTCTGCCTG

Exon 73700 to 73830

GTCTCTGTTTACCCTGATCTTCTTTTCTGCTGCAGAAACTGGATGCCCAGGTGA
GGCCGCGGTGGAGATGTATATTGAGGACTGGGTCATTGTCCACAGAAGGTG
 AGTCTGACTTAGGGGCAGCTCAGGGG

Exon 74010 to 74190

CCTGCCCAGCCCCGTTTCTGCTAGGTATCAGTACCTGAGTGCAGCATACAGC
CCCGTCACCACAGACACACAGCGGGAGCGACAGAAGGGCCTCCCCCGCCAG
GTCTTTGAGCAGGATGCTTCTGGAGACGAGAGGTCCGGCCCTGAGGACTCGG
 TGAGGAAGCCCCCTGGCTGGGGTCAC

Exon 75170 to 75450

CAGTGCTTGCACATTCTCCACTGGCAGAATGACTCCCGCGTGGCTCGGGCTC
CCCGGAAGACACCCCTCGAAGCAGTGGTGCCTCTAGCATCTTCGACCTGAGG
AACCTGGCAGCTGACTCATTGCTGCCCTCTCTGCTAGAGCGGGCGGCCCCAG
AAGATGTGGACCGGCGCAATGAAACCTTCGACGGCAGCACCGGCCCCCGGC
CCTGCTACCCCTCTACCCGGCACCTGACGAGGTGGGTGCCCTTCCAGATAT
 CAGCCAACCAGCATTTACT

FIG. 6A (1 of 7)

Exon 78100 to 78250

CCCGCCCAGCTCCCACCCCCCACTCTTGGCAGGATGAAGCCGTGGAACGCTG
TAGCCGCCCAGAGCCACCCCGCAGCACTTTGGACAAAGGATCTTGGTCAAG
TGTCTGTCGCTCAAGTGAGTATACTGACATGTCTCTCTTCTTAGATG

Exon 80380 to 80500

CCCCCTCCCTCCCATTTACTTGTAGGTTGAGATTGAAATTGAGCCCATCTTT
GGGATCTTGGCTCTGTATGATGTGCGGGAGAAAAAGAAGGTAGGAGGCCCTT
TTTTCTCTTTCTCCC

Exon 80540 to 80750

GTGGTGGCCCAGCTGCCTCTGGTGTCCCCAGATCTCGGAGAACTTCTACTTCG
ACCTGAACTCGGACTCCATGAAGGGGCTGCTTCGGGCTCATGGCACTGCCATCTCCACC
CTGGCCCGCTCTGCCATCTTCTCTGTGACCTACCCCTCACC
TGACATCTTCTGGTCATCAAGGTGCCTGCTGGGGCTGGGCAAGGGGGTGGT

Exon 82370 to 82510

GCCTCACTGGATTTCATTCATCTGCCCCGCAGTTGGAGAAGGTGCTTCAGCAAG
GGGACATCAGTGAGTGCTGTGAGCCTTACATGGTGTTGAAAGAAGTGGACAC
AGCCAAGGTAAGCGTGTGGAGGCTGGACTAGGGGCA

Exon 82540 to 82760

GCTGAGCTGGCAGGGGACGGGGTCTCCCCACAGAACAAGAGAAAGCTAGAG
AAGCTGCGCCTGGCGGGCCGAGCAGTTCTGCACCCGCCTGGGGCCGCTACCGCA
TGCCCTTCGCCTGGACGGCCGTGCACTTGGCCAACATCGTGAGCAGCGCTGG
GCAGCTGGACCGGGACTCTGACTCGGAGGGCGGTGAGGAGGCGGGGCTAAC
AGGCTTGGGGCGGGG

Exon 82860 to 83060

CTTGGTCCCCCTTTTGTCAATTGTCATTCCCTCCCCTAGAGCGCCGGCCAGCCT
GGACAGACCGCCCGCTCGGGGGCCCCAGGACCGGGCGAGTAGTGGGGACGACG
CCTGCAGCTTCTCTGGCTTCCGTCCAGCCACGCTAACTGTCACAACTTC
TTTAAGCAGGTGTCCTACCCTGGGGCCAGGGACTCTCCCACTCC

Exon 83100 to 83260

GCCCAGGCTGACGGGAGTGGGTCCCATGTAGGAGGCTGAGCGACTCAGTGAC
GAGGACCTCTTCAAGTTCCTGGCTGACATGAGGCGCCCGTCGTCCCTGCTGCG
GCGACTACGTCCCTGTGACTGGTGCGTGGCACACCCCATACACAAGAAGTATC
ACTC

Exon 84050 to 84270

GTGCAAACCGGTTCTTCCCTTCCCAGCCCAGCTCAAGATCGACATTTCTCCGG
CTCCTGAAAATCCCCACTTCTGCCTCTCCCCTGAGCTGCTTCATATCAAGCCC
TACCCGGACCCCAGGGGCCGGCCACCAAGGAGATTCTGGAGTTCCCCGCCC
GCGAAGTCTATGCCCCCATACAGCTACAGGTACGGCCTCTGGGGCCACAG
TGGGCACTTGA

Exon 87940 to 88130

GCCCCGTGCCCTCTGACACCCCCATCCTGCCCCCACAGGAACCTGCTGTACG
TGTACCCGCACAGCCTCAACTTCAGCAGCCGCCAGGGCTCCGTGCGCAACCT
TGCTGTGCGAGTGCAGTACATGACAGGCGAGGACCCAGCCAGGCTCTGCCG
GTCAGTGGCTGTGCCACAGGAAGGGGGGTAGGG

Exon 88140 to 88270

TGGGTCCCTCATGAATCCACTCTCCCAGGTCATCTTTGGCAAGTCCAGCTGCA
GTGAATTTACCCGCGAGGCCTTCACACCGGTGGTCTACCATAACAAGTATGT
AGGGGGACACGTGAGGAACCTTGGGGG

Exon 88470 to 88680

GCCCCAGCAGATCCCCCAGCCGATTCTGCCAGGTCCCCGAGTTCTACGA
GGAGTTCAAGCTGCATCTTCCAGCCTGCGTGACAGAGAACCATCACCTGCTG
TTACCTTCTACCATGTCAGCTGCCAGCCCCGGCCGGGCACTGCCCTGGAGAC
ACCCGTGGGCTTTACTGTGAGCCGTCCCCCTCCCTCCCTCCCCCTGAGCCCTCC
T

Exon 88680 to 88870

TCGTCCCCAACCTGGCCGCAGACCTGACCTCCAGCCTCTCCCCAGTGGATCC
CACTGCTGCAGCACGGGCGCTGAGGACCGGCCCTTCTGTCTCCCACTGCTC
GTGGACCAGCCGCCGCCAGCTATTCCGTGCTCACACCCGATGTATGTGCCCT
GGAGCTCCTGCCTGCCAATGCACTGTCCCCAG

Exon 89360 to 89530

CAGGGAGGGCTGACCAGTGCCACCTGGTGCCTCCCTCCCACAGGTGGCGCT
TCCGGGCATGCGCTGGGTGGACGGTCACAAGGGCGTGTTCAGTGTGGAGCTC
ACAGCCGTGTCTCTGTGCACCCCCAGGTACGGGGTGGGCCGGGAACCAAGA
GTCCCGCCCTGCTCC

Exon 89660 to 89980

TTCATTCCCTGAGGCCCCACCCTGCTCACTCCACATCCCTACCCAGGACCCCT
ACCTGGACAAATTCTTCACCCTGGTGCACGTCCTGGAGGAGGGAGCCTTCCC
ATTCCGGCTCAAGGACACTGTGCTGAGCGAGGGCAACGTGGAGCAGGAGCTG
CGGGCCAGTCTTGCAGCACTGCGCCTGGCCAGCCCCGAACCCCTTGTGGCCTT
CTCCCACCACGTGCTGGACAAGCTCGTGCGTCTGGTCATCAGGCCCCCGATC
ATCAGTGGCCAGATTGGTAAGCGAATGTGGCCTCAGACCTCAGTTTCCCCATC
CACATG

Exon 90480 to 90730

AGAGGCCTTGGGGCCTGGAACCTTGACCTCTGCTCTGCCCTGCAGTGAACCTG
GGCCGTGGAGCCTTTGAAGCAATGGCCCATGTAGTCAGCCTTGTTACCCGGA
GCCTGGAGGCAGCCAGGATGCCCGCGGTCACTGCCACAGCTGGCTGCCTA
CGTCCACTACGCCTTTTCGCCTTCCTGGCACTGAGCCAGCCTCCCGGATGGTG
AGTTTGTAGAAATCCCTGTGAGACGAGAAATATCTGGGAGAA

Exon 92870 to 93120

ATCACATCAGGTGGGTGGGTGGTTGACCCTATTCACTCCATCCTCAGGGGCCCC
TCCAGTGACAGTGACAGGCTGCCACACTGGCCCGTGGCTCTGGTCGCCCCGC
AAGCCTCTACCTGGCGCGTTCCAAGAGCATCAGCAGCAGCAACCCTGACCTC
GCCGTGGCCCCCTGGCTCTGTGGATGACGAGGTTTCCCGCATCCTGGCCAGCA
AGGTAGGGCAACGGGGGCCCTGGAATCTCCAGCCTCAGTGGT

Exon 97210 to 97390

GGCACCTCGCACTCTGTGACCCCTGCCTCTGTCCCCAGCTGCTTCACGAGGAG
CTGGCTCTGCAGTGGGTGGTCAGCAGCAGTGCCGTACGCGAGGCCATCCTCC
AGCACGCCCTGGTTCTTCTTCCAGCTCATGGTGAGACCCCTCCTCCCTGCCTG
GTGGCAAGAGACCCCACTGGAG

Exon 98770 to 98990

CAAATCCCACCCACAGCCCTCTCACCCACCCCAAGGTGAAGAGTATGGCGC
TGCACCTGCTGCTTGGCCAGCGACTAGACACACCCCGCAAGCTGCGCTTCCC
CGGACGCTTCTTGGACGACATCACTGCCTTGGTGGGCTCTGTGGGCTGGAG
GTCATCACCCGTGTCCACAAGGTGAGAGATGCAGGGTCTCAATGTGGGAAGA
AACCTGAGGGAGG

Exon 103130 to 103340

GGGGCTGAGGTTTGGGTGTGTGGGTTGACAGGCACCTGTGTCCCAGGATGT
GGAGCTGGCCGAGCACCTCAACGCCAGCCTGGCTTTCTTCTCAGTGACCTTC
TGTCCCTGGTGGACCGGGGCTTTGTCTTCAGCCTGGTCCGGGCCCCACTACAAG
CAGGTAGGAGTGGGCGTGGGCAGGGTGGGCATGGCATGGATGGAAGCGGGA
GC

FIG. 6A (4 of 7)

Exon 103340 to 103590

CAATGTTGACATCACTGATGGCCACCCCTCTCCTGCAGGTGGCCACGCGGCT
CCAGTCGTCCCCTAATCCAGCAGCCCTGCTGACCCCTGCGCATGGAATTACCCG
CATCCTGTGCAGCCACGAGCACTACGTGACCCCTCAACCTCCCCTGCTGCCCCC
TGTCACCTCCAGCCTCGCCCTCCCCCTCTGTGTCTCCACCACCTCCCAGGTG
GGCTGCCTTCACTTCTGCCTCCTCTCTTTGACCTACAAC

Exon 103990 to 104220

TGACCCCTTGACCGCTGGCATCCCCATTTTTCCCCACTCTGCAGAGCTCCAC
CTTCTCCAGCCAAGCCCCGGACCCCAAGGTGACCAGCATGTTCGAACTGAGT
GGACCATTCGCGCAGCAGCACTTCCTAGCTGGGCTCCTGCTGACGGAGCTGG
CACTGGCCCTCGAACCTGAGGCTGAAGGGTGAGCAGAGCTCCTGTCTAGCCCC
AGGACAGGTGGGACAGTCCAG

Exon 104220 to 104480

GGAGCCATGTCCACCCTGTCCTGAGCACCTCATTACCCCATAGGGCATTCCTG
TTGCACAAGAAGGCCATCAGTGCTGTGCACAGCCTGCTATGTGGCCATGACA
CTGACCCCCGCTACGCCGAGGCCACTGTGAAGGCTCGTGTGGCCGAGCTGTA
CCTGCCACTGCTATCGATTGCACGGGATACCTTGCCACGGCTGCATGACTTTG
CTGGTCAGTGGGCCAGGGGAAGATGGGGTCACATGATCCAGGGACTTGGTG

Exon 108850 to 109100

ACCAAGGGTTTATCTTTCTTTCCCTCTGTCTTTCCCTGCCAGAGGGCCCAGGTC
AGCGGTCAAGACTGGCCTCAATGCTTGACTCAGACACAGAAGGCGAAGGGG
ACATTGCGGGTACCATCAACCCCTCTGTGGCCATGGCCATTGCTGGTGGCCCCC
TAGCCCCCTGGCTCCCGGGCCAGCATCTCCAGGGGGCCACCAACGGTGAGTA
GGGAGGCTTGTCCTCATAGACATCATCCACTTTGAATGAGA

Exon 109140 to 109410

TCACATGGAGAAAATGGAAATTGACTTTGATTCTCTCTGGCCCCAGGCTTCT
CGCGCAGGCTGTGCCCTCTCTGCTGAGTCAAGCCGGACCTTGCTGGCGTGTGT
GCTGTGGGTGCTGAAAAACCCGAGCCGGCGCTCCTGCAGCGCTGGGCCACT
GACCTGACACTCCCCCAGCTGGGACGTCTGTTGGATTGCTGTACCTTTGCCT
AGCTGCCTTTGAGTACAAGGTTTGAGGGCGTGGGCAGGAGATGATGGAGGAG
GCAGGCTA

FIG. 6A (5 of 7)

Exon 110310 to 110530

GAAAAGAGCAGAGTCAGCCTGGAACCCAGTTCTCTGCACCCCCAGGGGAA
AAAGGCCCTTTGAACGCATCAACAGCCTCACATTCAAAAAATCTCTGGATATG
AAGGCGCGGCTAGAGGAAGCCATTCTGGGTACCATCGGAGCTCGACAAGAA
ATGGTTCGGCGAAGTCGTGCTAAGAGGGTGACATACCCACGTGTCCCCATCC
CACCAGCTGCTCCCA

Exon 110770 to 110940

TGTGTTTTTACGCATCTGTGATCGTGACCCACGCGTCTCAGAGAGGAGCCCC
TTTGGGAATCCGGAGAATGTGCGCTGGCGGAAGAGCGTCACACACTGGAAGC
AAACCTCAGACCGCGTGACAAGTAGGTGTGGGCAGGAGGGTGTCTGCTGAG
TTCAGAACAGTTTG

Exon 111590 to 111770

ATCTCACCCCGAGTGGGCCCCCAAGACCTCCTTTCCCTTCCAGGACCAAGG
ATGAAATGGAACACGAGGCCCTTGGTGGGAAGGGAACCTGGCAACCGAGGCAA
GCCTAGTGGTTCTGGACACACTGGAGATCATCGTGCAGGTAGGGCTTGATCC
AGCATCTGCCTTGTGCTCTGAGCCCA

Exon 111830 to 112050

ACCCTAGGCTCTAACACCTGGATTCTTGACCCCTTCCCTCCAGACGGTGATG
CTTTCAGAAGCCCGGGAGAGCGTCTTGGGGGCAGTGCTGAAGGTTGTGCTGT
ACAGCCTGGGCAGTGCCAGAGTGCCCTCTTCTTGACGATGGCCTGGCCAC
CCAGAGGGCCCTTGTGTCCAAGGTGAGCACCCTCAACAACCATGATTCTTA
GAAAAACAGTAG

Exon 112910 to 113140

AACGGGGAGGGGCTGGACAGTGTCTGTCTGGGTCCCTTGGGGGCAGTTCCCGG
AGCTGCTGTTTCGAGGAGGACACGGAGCTGTGTGCCGACCTGTGCCTGAGGCT
CCTACGACACTGTGGCAGCCGCATCAGCACCATCCGCACGCACGCCAGCGCC
TCGCTGTACCTGCTCATGCGACAGAACTTCGAGATCGGCCACGTGAGTGGGG
GCTAGGAGGCATGGTCCACACATGGCTCTGGTC

Exon 114090 to 114340

TCTGAGACTCCCGGCTCCACCCTCCCGCCCCTGTCCCTGCAGAACTTTGCCCC
TGTGAAGATGCAGGTCACCATGTCTCTCTCGTCCCTGGTGGGGACGACGCAG
AACTTCAGTGAAGAGCACCTGCGACGTTCACTCAAAACCATCCTCACCTATG
CTGAGGAGGACATGGGGCTGCGGGACAGCACCTTCGCAGAGCAGGTGACAC
CTGCTGGGTCCCCGCCCCGCTCCCTTCATATAACTCCCAAC

FIG. 6A (6 of 7)

Exon 114370 to 114550

ATGCTCTCATTGGCCCCCTGGACGTTCCCCGGCTCCAGGTCCAGGACCTGATGT
TCAACCTGCACATGATCCTGACGGACACGGTGAAGATGAAGGAACACCAGG
AGGACCTGAGATGCTCATCGACCTCATGTACAGGTGAGGTGGGCCAGCTGG
CACCTTCAGCCACGCCCACGCCCA

Exon 116900 to 117170

AGGTGAGTCCCCTCCTCACATCCCCCTCACCTGGACTCCAGAATTGCCCGGG
GCTACCAGGGCTCACCGGACCTTCGGCTGACCTGGTTGCAGAACATGGCCGG
GAAGCACGCGGACGTGGGCAACCACGCCCAGGCCCGCCAGTGCATGGTGCA
CGCGGCCGCCCTCGTGGCTGAGTACCTCGCCCTGCTCGAGGACCAGCGCCAC
CTGCCCCGTGGCTGGCGATTTCCTTCCAGGTGAGTGGCCAGGGGTGGCAGGT
GGCGGACGGCA

Exon 117170 to 117410

ACGAGTGCAGTGGGGACCAGGGTCTGACGCCACCTCTCCCACCCAGAACAT
CTCATCCAACGTGCTAGAGGAGTCCGCCATCTCCGACGACATCCTGTGCCCC
GACGAGGAGGGCTTCTGCTCCGGGAAGCACTTCACTGAGCTGGGGCTGGTAG
GGTTGCTGGAACAGGCAGCCGGCTACTTCACCATGGTGAGGCCTTGGGGACT
GGGTGCAGGAGAGGGGGCTCGGGCCAGGGAGGT

Exon 121670 to 121900

GAGAGGAAGACAGTTTGGGGAATCCTGACCCACCTCACCCTCAGGGCGGGC
TCTACGAGGCGGTGAATGAGGTCTACAAGAACCTCATCCCCATCCTGGAAGC
CCACCGTGACTACAAGAAGCTGGCCGCGGTGCACGGCAAACCTGCAGGAGGC
CTTACCAAGATCATGCACCAGGTGGGCCCAGGACCCCTCCCCAGACCCCA
CCCTCAGCCCCACTCCTCATCC

Exon 121910 to 122000

CCCCAGGGATCTGCTGACCTTGACCCTTCTCTTCCCCACAGAGTTCGGGTGG
GAGGTGAGTCAGCCTTGGTGGACAGCCACCTGCCTCTG

Exon 123290 to 123510

TCCAGCAGGGGCCTCCCGGACAACCACACCCTTCTCACAGCCCCAGCGGT
GTTCCGGACGTATTTCCGCGTGGGCTTCTACGGCGCCCACTTCGGTGACCTGG
ATGAGCAGGAGTTTGTGTACAAGGAGCCATCGATCACGAAGCTGGCAGAGAT
CTCACACCGGCTGGAGGCATGTCCTTGTGTTGGGGGTGGAACGGGGCATGG
GGCTGCCTTGGG

Exon 123510 to 123633 (end clone)

GGCTGGAGTAGGGGCTGTCCCTGGGTGGCCCCGAGTCAGCCCTGTGTCTCCA
GGAGTTCTACACGGAGAGATTGGCGACGACGTCGTTGAGATTATCAAAGAC
TCTAACCTGTGGACAAGTC

FIG. 6A (7 of 7)

GGGCATGTGGCTCATTCTGTAATCCCGGCACTTTGGGAGGCGGAGGCGGGTGGATC
 ACCTGAGGTGAGGAGCTCCAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTAC
 TAAAAATACAAAAATTAGCCAGGTGTGATGGTGGGTGCCTGTAATCCCAGCTACTC
 GGGAGGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCAGAGGTTGCGGTGAGCC
 GAGATTGTGCCATTGCACTCCAGTCTGGGCAACAAGAGCGAAATGCCACCTCAAAAT
 AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAGAGGATAA
 AATGCCAGCAACCCATAGATGGGAATGAGAACAGCACGTGCAAAGGCCCTGAGGCA
 GAGCCACGGCCTTGTCTGATTCAACCTCAAATTCTCCCTGGGGCATTGTGCTGACCAGG
 GAAAGAAGGGCTGTCCAGGAGGAAGGACCTGCCGGTGCAGAGGCATGCAGGTGAGA
 AAGGGGTGAGCTCCTCCAGAGGGGAGTGTGGCTGGAGAATTCTCTAAAAATGCTGC
 AGCAGTGTGGGAGAGAGGCCAGTGGGGAGAGATTTGAGACCATAGATTAACCAAG
 ACATCCCCACCTCTTCTCTTGGTAGAGGCGGCCCGAAAGTCTAGACTCCCAAACT
 GGCTCACTCAGGTCCCACCTGGACCTGGGGCACATCTCCGAGCACTCCAGTGCC
 TAGCCAGGCTCCTCTGACTCCCATGCTGTAGACTGGGAGCACGGACAATGCAGGCGC
 TGGAGACCCCTGTGAGTCACACTGAGCAAGCACCCGAACACCTCTGTGCCTCAGTTT
 ACTCATCTGTAAAAGGAGGAAAACAATAATTTCTTCTGCATGTGTGAATTGCAGGGC
 CAGGCTCAATGACATCTTAGCAATTAGACTTTTTGAGACAGGGTCTCGCTCTGTACC
 CAGGCTGGATTGAAATGGCAATCACAGCTCACTGCAGCCTTGACCTCCCAGGCTC
 AAGCGATCCTCCTCCTCAGACTCCCAAGTAGCTGAGATTACAGGCACACACCACCA
 TGCCTGGTTAATTTTGCATTTTTTGTGGACACGGGGTCTCATTATGTGCCCAGGCT
 GGTCTCCAACCTCCTGGGCTCAAACAATCCTCCTGCCTTGGCCCCCACAGTGTGGG
 ATTACAGGCATGAGCCACCATGCACGGCCACGATTATACTTACAGGTATGATTATTA
 GATACATGAACATCGTTATTGTTTTCCAGCCAGGAGTCAGAGGGCAGAAAGAGCGCC
 CCCCAAACCCCGGAAATCTGGGGCCTACCCAGCCTGGGTCCCAGCGCCTCCCTCCC
 TCCCTCCTCCTGAGCTTCAGTTTCCCCAGCCCTGCTCCTGGGGTGGTAAGACCACCC
 CACTAAACCCCGGGAGCCTGGGGTCCACCTAGCCCGGGTCTCAGCGCCTCCCTCCC
 TCCCTCCCTCCTCAGGCTCAGTTTCTCCAGCCAGCTCCCAGGGTGAAAGAGCGCC
 CCCGCCAGCTCGGGAGTCTGGGGCACCCCAAGTCTGGGTCCCAGCGCCTCCTCTCCC
 TAACTTCCCTCCTCAGCCTCAGTTTCCCCAGCCCTTCTCCTAGGGTAGAAAGAGCGTC
 CCCCCAGCCCGGGAGTCTGGGGCCCGCCAGCCTGGATCCCGGGGCTCCTCTCCGT
 CCCCAGCCTCAGTTTCCCCAGCCCCAGGACTCCAGGCGACCCCTCCGGCTGCAGG
 GGCAGCACGGAGCGGCCCGGGCCACCCGGAAGGGCCCCGCCCCGCGCCGCCCCG
 CCCCCGCCCCGGCTGCCCAGAACCGGGAGGCGGGCGGGCGGGCGGGGCCCCG
 GGGCGGCGGGCGGGACGCGAGGACCATGGCTGCCTCCGAGCGCCGCGCCTTCGC
GCACAAGATCAACAGG

FIG. 6B

```

hCLASP4 -----MFPMEDISISVIGRQRRTVQ----- 20
hCLASP5 -----MTHLNSLDVQLAQELG----- 16
hCLASP3 -----MAERRAFQAKISRTVAAAEVRKQISGQYSGSPQLLKNLNI 41
hCLASP2 -----MLLFYPYDDFQTAILRRQGRYICS----- 23
hCLASP7 -----MAASERRAFQAKINRTVAAAEVRKQVSRERSGSPHSSRRCSS 43
hCLASP1 MSFRGKVFVKREPSEFWKKRRTVRRVIOEEFHRFSQEKPRLLEPLDYETVIEELEKTYRN 60
      . . .

hCLASP4 -----STVPEDA EKRAQSLFVKECIKTYSTDWHVVNYK 53
hCLASP5 -----DFT 19
hCLASP3 N-----ISHHTTVPLTEAVDPVDLEDYLI THPLAVDSGPLRDLIEFP 83
hCLASP2 -----TVPKAE EEAQSLFVTECIKTYNSDWHVLVNYK 55
hCLASP7 G-----VPLTEVVEPLDFEDVLLSRPPDAEPGLRDLVEFP 79
hCLASP1 DPLQDLLFFPSDDFSAATVSWDIRTLYSTVPEDA EHKAE NLLVKEACKFYSSQWHVVNYK 120
      : :

hCLASP4 YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED-----SSSLCSQKGGVIKQG 105
hCLASP5 DDDL DVVFTPKECRTLQP-SLPEEGVELDPHVR-----DCVQTYIREWLI 63
hCLASP3 PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI 126
hCLASP2 YEDYSGEFRQLPNKVVKLDKLPVHVVEVDEEVDKDED-----AASLGSQKGGITKHG 107
hCLASP7 ADDLELLLQPRECRTEP-GIPKD-EKLD AQVR-----AAVEMYIEDWVI 122
hCLASP1 YEQYSGDIRQLPRAEYKPEKLP SHSFEIDHEDADKDEDTTS HSSSKGGGAGGTGVFKSG 180
      : : . : * . : * .

hCLASP4 WLHKANVNSTIT--VTMKVF KRRYFYLTQLPDGSYILNSYKDEKNSKESK-GCIYLDACI 162
hCLASP5 VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAQA--GPRHLNVLC 118
hCLASP3 VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGN SYQDDQLKRRSMSI 183
hCLASP2 WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDGSYNLNFYKDEKISKEPK-GSIFLDSCM 164
hCLASP7 VHRRYQYLSAAY--SPVT TDTQRRERQKG-LPRQVFEQDASGDERSGPDSDNDSRRGSGSP 179
hCLASP1 WLYKGNFNSTVNNTVTVRSFKKRYFLTQLPDNSYIMNFYKDEKISKEPK-GCIFLDSC 239
      : : . : * : : . : .

hCLASP4 DVVQCPKMRRHAFELKMLDKYSHYLA AE TEQEME EWLITLKKIIQINTDSL VQEKKETVE 222
hCLASP5 DVSGKG PVTACDFDLRSLQPDKRLNLLQQVSAEDFEKQNEEARRTN-----RQAE 169
hCLASP3 DDTPRGSWACSI FDLKNSLPDALLPNLLDRTPNEEIDRQND DQRKSN-----RHKE 234
hCLASP2 GVVQNNKVRREFAFELKM QDKSSYLLAADSEVEME EWITILNKILQLN-----FEAAMQEK 219
hCLASP7 EDTPRSSGASSI FDLRNLAADSL LPSLLERAAPEDVDRRNETLRQH-----RPPA 230
hCLASP1 GVVQNNRLRKYAFELKMNDLTYFVLAETESDMDEWIHTLNRILQISPEGPLQGRRSTEL 299
      * : : . : :

hCLASP4 TAQDDETSS----QGKAENIMASLERSMHP ELMKYGRETEQLNKLSRGDGRQNLFSFDSE 278
hCLASP5 LFALYPSVD----EEDAVEIRPVPECPKEHLG-----N-----RILVKLLTLKFEIE 212
hCLASP3 LFALHPSPD----EEEP IERLSVPDIPKEHFG-----QRLLVKCLSLKFEIE 277
hCLASP2 RNGDSHEDD----EQSKLEGSGSGLSYLP ELAKSAREAEIK--LKESERVKLFYLDPD 272
hCLASP7 LLTLYPAPD----EDEAVERCSRPEPPREHFG-----QRLVKCLSLKFEIE 273
hCLASP1 TDLGLDSLNSVTCECTPEETDSS ENNLHADFAKYLTETEDTVKTTNRMERLNLFSLDPD 359
      . : : : :

hCLASP4 VQRLDFS----GIEPDIKP-FEECKNKRFLVNCHDLTFN ILGQIGDNAKG PPTNVEPFFI 333
hCLASP5 IEPLFAS----IALYDVKERKKI SENFHC DLNSDQFKGFLRAHTPSVAASSQARS AVFSV 268
hCLASP3 IEPIFAS----LALYDVKEKKK ISENFYFDLNS EQMKGLLRPHVPPAAITTLARSAIFSI 333
hCLASP2 AQKLDFS----SAEPEVKS-FEEKFGKRILVKCNDSL FNLQCCVAENE EGPTTNVEPFFV 327
hCLASP7 IEPIFGI----LALYDVREKKK ISENFYFDLNS DSMKGLLRAGHTHPAISTLARSAIFSV 329
hCLASP1 IDTLKLQKKDLLEPESVIKPFEEKAAKRIMIICKALNSNLQGCVTENENDPITNIEPFFV 419
      : : . : . : . : . : * :

```

FIG. 7 (1 of 6)

[illegible]

FIG. 7 (2 of 6)

hCLASP4	FKSHLESTIYTQDLHVHKFFHHCQLIQS-----GSKEVPGELIKYLKCLHAM	794
hCLASP5	IEVQAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHELKLSIICLNSS	715
hCLASP3	VEVVAVSSIHTQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLENELKSSISALNSS	780
hCLASP2	ISTHLVSTVYTQDQHLNFFQYCQKTES-----GAQALGNELVKYLKSLHAM	787
hCLASP7	VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLSEGNVEQELRASLAALRLA	767
hCLASP1	VSTFVVSTVNTQDPHVNAFFQECQKREK-----MSQSPTS NFIRCKNLLNVE	887
	.. *::.* *::.* *::.* *::.*	
hCLASP4	EIQVMIQFLPVILMQLEFR-----VLTNMTH-----EDDVP	824
hCLASP5	RLEPLVLFHLVLDKLFQLSVQPMVIAGQTANFSQFAFESVVAIANSLHNSKDLSKDQHG	775
hCLASP3	QLEPVVRFLHLLDKLILLVIRPPVIAGQIVNLGQASFEAMASIINRLHKNLEGNHDQHG	840
hCLASP2	EGHVMI AFLPTILNQLFR-----VLT-RAT-----QEEVA	816
hCLASP7	SPEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGAFEAMAHVSVLHRSLEAAQDARG	827
hCLASP1	KIHAIMSFLPIILNQLFK-----VLVQNE-----EDEIT	916
	.::.* *::.* *::.*	
hCLASP4	INCTMV-LLHIVSKCHEEGLDS-----YLRSFIKYS-----FRPEKP	860
hCLASP5	RNCLLASVYHVFRLEPEVQRDPKSGAPTALDPRSHTYGRTSAAAVSSKLLQARVMSS	835
hCLASP3	RNSLLASYIHVFRLPNTYPNSSSPG-PGGLGGSVHYATMARSAVRPASLNLNRSRSLN	899
hCLASP2	VNVTRV-IIHVVAQCHEEGLES-----HLRSYVKYA-----YKAEPY	852
hCLASP7	HCPQLAAYVHYAFRLPGTEPSLPDGAPP---VTVQAATLARGSGRPASLYLARSKSISS	883
hCLASP1	TTVTRV-LPDIVAKCHEEQLDH-----SVQSYIKFV-----FKTRAC	952
	. . . :	
hCLASP4	SAPQAQLIH-----ETLATTMIAILKQS-----	883
hCLASP5	SNPDLAGTHSAADEEVKNIMSSSKIADRNC SRMSYYCSGSSDAPSSPA-----	882
hCLASP3	SNPDISGTPTSPDDEVRSIIGSKGLDRSNSWNTGGPKAAPWGSNPSPSAESTQAMDRSC	959
hCLASP2	VASEYKTVH-----EELTKSMTTILKPS-----	875
hCLASP7	SNPDLAVAPGSVDDEVSRILASKLLHEELA-LQ-----	915
hCLASP1	KE---RPVH-----EDLAKNVTGLLKS-----	972
	: . .	
hCLASP4	-----ADFLSINKLLKYS-----WFFFEIIAKSM	907
hCLASP5	-----APRPASKKHFEELALQ-----MVVSTGMVKSM	910
hCLASP3	NRMSSHTETSSFLQTLTGRLP TKKFHEELALQWVVC SGSVRESALQAWFF FELMVKSM	1019
hCLASP2	-----ADFLTSNKLLRYS-----WFFFDVLIKSM	899
hCLASP7	-----WVVSSSAVREAILQHA-----WFFFLQMVKSM	942
hCLASP1	-----DSPTVKHVLKHS-----WFFFAIILKSM	995
	. * . . : ***	
Cadherin Cleavage		
hCLASP4	ATYLLEENKIKLERGQREFPETYHHVLSLLLAIPHVTIRYAEIPDE---SRNVNYSLAS	964
hCLASP5	AQHVNMDKRDSEFRRTRFSDRFMDITTIVNVVTSEIAALLVKPKENEQA EKMNISLAF	970
hCLASP3	VHHLYFNDKLEAFKSRFPERFMDIAALVSTIASDIVSRFQKDTM---VERLNTSLAF	1076
hCLASP2	AQHLENSKVKLIRNQREFASYHHAAETVVNMLMPHITQKFGDNPEA---SKNANHS LAV	956
hCLASP7	ALHLLLGQRLDTERKLEFPGRFLDDITALVGSVGLVITRVHKDVEL---AEHLNASLAF	999
hCLASP1	AQHLIDTNKIQLERPORFPESYQNELDNLMVLS DHVIWKYKDALEE---TRRATHSVAR	1052
	.::.* *::.* *::.* *::.* *::.* *::.*	
hCLASP4	FLKRCCLTMDRGFIENLINDYISGFSPKDP-----KVLAEYKFEFLQTICNHEHYIPLNL	1019
hCLASP5	FLYDLLSLMDRGFVENLIRHYCSQLSAKLSNL---HTLISMRLFEFLRILCSHEHYLNLNL	1027
hCLASP3	FLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVLVSLRLDFLRICSH EHYVTNLNL	1136
hCLASP2	FIKRCFTFMDRGFVKQINNYISCFAPGDP-----KTLFEYKFEFLRVVCNHEHYIPLNL	1011
hCLASP7	FLSDLLSLVDRGFVFSLVRAHYKQVATRLQSSPNPAALLTLRMEFTRILCSHEHYVTNLNL	1059
hCLASP1	FLKRCFTFMDRGCVFKMVNNYISMFS S GDL-----KTL CQYKFDLQEV CQHEHFIPCL	1107
	: .::. *::.* *::.* *::.* *::.* *::.*	

FIG. 7 (3 of 6)

Cadherin EC motif

hCLASP4	PMAFAKPKLQR-----VQDS--NLEYSLSDEYCKHHFLVGILLRETSI	1060
hCLASP5	FFMNADTAPTSP--CPSISSQNSSSSCSFQDQKIASMFDLTSEYRQQHFLTGLIFTELA	1085
hCLASP3	PCSLLTTPASPSPSVSSATSQSSGFTSNVQDQKIANMFELSVFPRQQHYLAGIVLTELAV	1196
hCLASP2	PMPFGKGRIQR-----YQDL--QLDYSLTDEFCRNHFLVGILLREVGT	1052
hCLASP7	PCCPLSPASPSPSVSSTSQSSTFSQAPDPKVTSMFELSGPFRQQHFLAGILLTELAL	1119
hCLASP1	PIRSANIPDPLTP-----SES----TQELHASDMPEYSVTNEFCRKHFLIGILLREVGF	1157
	. : : : : : * : * : *	
hCLASP4	ALQDN----YEIRYTAISVIKNLLIKHAFDTRYQHKNQQAIAQLYLPFVGLLLENIR	1116
hCLASP5	ALDAEGEGISKVQRKAVSAIHSLSSHDLDPRCVKPEVKVIAALYLPVGIILDALP--	1143
hCLASP3	ILDPDAEGLFGLHKKVINMVHNLSSHSDSPRYSDPQIKARVAMLYLPLIGIIMETVP--	1254
hCLASP2	ALQEFR----EVRLLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVORI	1108
hCLASP7	ALEPEAEGAFILHKKAISAVHSLLCGHDTDPRYAEATVKARVAELYLPLLSIARDTLP--	1177
hCLASP1	ALQEDQ----DVRHLALAVLKNLMAKHSFDDRYREPRKQAQIASLYMPLYGMLLDNMPRI	1213
	* : : : : : * * * : : : * * : *	
hCLASP4	AGRDTLYSCA-----AMPN-S----ASRDEFPCGFTSPANRGSLSLTDKDTAYGS	1160
hCLASP5	-----QL-----CDFTVADTRRYRTSGSD----	1162
hCLASP3	-----QLY-----DFTETHNQGRGPCIATDD--	1276
hCLASP2	NVRDVSPFPVNAAGMTVKDESLALPA-VNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTT	1167
hCLASP7	-----RLH-----DFAEGPGQSRSLASMLDSLTE	1201
hCLASP1	YLKDLYPFTVNTSNQGSRDDSLSTNGGFQSQTAIKHANSVDTSFSKDVLSNSIAAFSSIAIS	1273
	. : .	
hCLASP4	FQ-NGHGIKREDSRGS LIPEGATGFPDQNGTGEN-----TRQSSTRSSVSQYNRLDQYE	1213
hCLASP5	-----EEQEGAGAINQNVALAIAGNNFNLKT-----SGIVLSSLPYKQYNMLNADT	1208
hCLASP3	-----YESESGSMISQTVAMAIAGTSVPQLTR---PGSFLTSTSGRQHTTFSAES	1324
hCLASP2	STPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSSVVRCDKLDQSE	1227
hCLASP7	-----GEGDIAGTINPSVAMAIAGGPLAPGSR---ASISQGPPTASRAGCALSAES	1249
hCLASP1	-----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPLALIGSTLRFDRLDQAE	1327
	. : . : .	
hCLASP4	IRSLLMCYLYIVKMISEDTLLTYWNKVSPQELINILILLEVCLFHFYRMGKRNIARVHDA	1273
hCLASP5	TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLLFICVLCFEYKGKQSSDRVSTQ	1268
hCLASP3	SRSLLICLLWVLKNADETVLQKWFDTLSVLQLNRLLDLLYLCVSCFEYKGKQVFERMNSL	1384
hCLASP2	IKSLLMCFLYILKSMSDDALFTYWNKASTSELMDEFTISEVCLHQFQYMGKRYIARNOEG	1287
hCLASP7	SRTLLACVLWVLKNTTEPALLQRWATDLTLPQLGRLLDLLYLCLAAFEYKGKKAFAFEHINS	1309
hCLASP1	TRSLLMCFLHIMKTISETLIAYWQRAPSPPEVSDFFSILDVCLQNFYRLGKRNIIRKIAA	1387
	. : * * : * : : : : : : * * * : *	
hCLASP4	WLSKHFGIDR-----KSQTMPALNRNSGVQARLQHLSSLESS-----	1311
hCLASP5	VLQKSRDVKAR-----LEEALLRGEARGEMMRRRAPGNDRFPGLNEN---	1311
hCLASP3	TFKKSMDMRK-----LEEAILGSIGARQEMVRRSRGQLERSPSGSAFGSQ	1430
hCLASP2	LGPIVHDRKS-----QTLPVSRNRTGMMHARLQQLGSLDNS-----	1323
hCLASP7	TFKKSMDMKAR-----LEEAILGTIGARQEMVRRSRERSPPFGNPEN----	1350
hCLASP1	AFKFVQSTQNNGTLLKGSNPSCQTSGLLAQWMHSTSRHEGHKQHRSTLPIIRGKN----	1442
	. : .	
hCLASP4	-----FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFETQCFKTQLL	1359
hCLASP5	--LRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAHLIILDMQENIQASS-ALD	1368
hCLASP3	ENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEANLIILDTLEIVQTVS-VTE	1489
hCLASP2	-----LTFNHSYGHSDADVHLQSLLEANIATEVCLTALDTLSLFTLAFKNQLL	1371
hCLASP7	--VRWRKSVTHWKQTSRDRVDKTKDEMEHEALVEGNLATEASLVVLDLTLIIVQTVM-LSE	1407
hCLASP1	--ALSNPKLLQMLDNTMTSNSNEIDIVHHVDTEANIATEGCLTILDVLSLFTQTHQRQLQ	1500
	. : : : : * * * * * * * *	

FIG. 7 (4 of 6)

hCLASP4 NNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIKSFPSAFFKGRVNMCAAFCY 1419
hCLASP5 CKDS---LLGGVLRVLVNSLNCDSQSTYTLTHCFATLRLAIKAFGDLLEEEVEQCQFDLCH 1425
hCLASP3 SKES---ILGGVLKVLHSMACNQSAVYLQHCFAQTRALVSKFPELLFEEETEQCADLCL 1546
hCLASP2 ADHGHNPLMKKVFDEVYLCFLQKHQSETALKNVFTALRSLYKFPSTFYEGRADMCAALCY 1431
hCLASP7 ARES---VLGAVLKVVLVYSLGSAQSALFLQHGGLATQTRALVSKFPELLFEEDTELCADLCL 1464
hCLASP1 QCDCQNSLMKRGFDTYMLFFQVQNQSATALKHVFASLRLVCKFPFAFFQGPADLCGSFCY 1560
.: : : : ** * : : : * : : ** . : : . : * : *

hCLASP4 EVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTHLQIIIAVSQLIADVALSGG 1479
hCLASP5 QVLHHCSSSDMVTRSQCACATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 148
hCLASP3 RLLRHCSSSIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVPMSLSSLVGTSQNFNE 1604
hCLASP2 EILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFRVTHLQVIISVSQLIADVVGIG 1491
hCLASP7 RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGHNFARVKMQVTMSLSSLVGTTQNFSE 1522
hCLASP1 EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSQLIADAG-IGG 1619
.:*: * :... **:** .: .: * :*: :*:.*: .

hCLASP4 SRFQESLFIINNFAHDRPMKATAFFAEVKDLTKRIRTVLMATAQMKHEKDPEMLIDIQ 1539
hCLASP5 EHLRSLRLTILAYSEEDTAMQMPPTQVEELLNLNSILYDVTVMREFQEDPEMLMDIM 1543
hCLASP3 EFLRSLKLTILTYAEEDLELRETTFPDQVQDLVFNLMILSDTVKMKEHQEDPEMLIDIM 1664
hCLASP2 TRFQQSLSIINNCANSRLIKHTSFSSDVKDLTKRIRTVLMATAQMKHEHNDPEMLVDLQ 1551
hCLASP7 EHLRSLKLTILTYAEEDMGLRDSTFAEQVQDLMFNLMILTDTVKMKEHQEDPEMLIDIM 1582
hCLASP1 SRFQSLAITNNFANGDKQMKNSNFAEVKDLTKRIRTVLMATAQMKHEKDPEMLVDLQ 1679
.:** : : * : : * :*: * : : * :*: * :*:**

transmembrane

hCLASP4 YSLAKSYASTPELRKTWLDMAKIHVKNGLFSEAAMCVVHVAALVAEFLHRRK----- 1592
hCLASP5 YRIAKSYQSPDLRLTLWLQNMAEKHTSKKCYTEAAMCLVHAAALVAEYLSMEDH----- 1598
hCLASP2 YRIAKGYQTSPE-RLTWLQNMAGKHSRSHAEAAQCLVHSAALVAEYLSMEDR----- 1718
hCLASP7 YSLAKSYASTPELRKTWLDSMARIHVKNGLDSEAAMCVVHVTALVAEYLTRKG----- 1604
hCLASP1 YRIARGYQGSPLRLTLWLQNMAGKHAELGNHAEAAQCMVHAAALVAEYLLLEDQ----- 1637
YSLANSYASTPELRRTWLESMAKIHARNGLDSEAAMCYIHIAALIAEYLLRKGYYKWKVEKI 1739
* :.* :*: * **:.** . :*** * :* :*.***:

hCLASP4 -----LFPNGCSAFKKITPNIDEEGAMKEDAGMMD----- 1622
hCLASP5 -----SYLPVGSVSFQNTSSNVLEESVVSIEDTLSPDEDGV 1633
hCLASP3 -----KYLPGVCVTFQNTSSNVLEESAVSDVVSPDEEGI 1753
hCLASP2 -----VFRQGCTAFRVTITPNIDEASMMEDVGMQD----- 1634
hCLASP7 -----RHLPGVCVSFQNTSSNVLEESAISDDILSPDEEGF 1672
hCLASP1 CTASLLSEDTHPCDSNSLLTTPSGGSMFSGWPAFLSITPNIKEEGAAKEDSGMHD----- 1795
: * : * :*: ** . : *

ITAM

hCLASP4 ---VHYSEEVLELLEQCVDDLWKAERYEIISEISKLVPIYEKRREFEKLTVYRTIHG 1679
hCLASP5 CAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLVIPILEAHREFRKLTLTHSKIQR 1693
hCLASP3 CSGKYFTESGLVGLLEQAAASFMSMAGMYEAVNEVYKLVIPILEANRDAKKLSTHKGKIQE 1813
hCLASP2 ---VHFNEDELVMELLEQCADGLWKAERYELIADIYKLIPIYEKRR----- 1677
hCLASP7 CSGHFTDELGLVGLLEQAGFYTMGGLYEAVNEVYKLVIPILEAHRDYKKLAAVHKGKIQE 1732
hCLASP1 ---TPYNENILVEQLYMCGEFLWKSERYELIADVKNKPIIAVFKEQRDFKKLSDIYYDTHR 1852
:. * : * . : . ** : : : * : : : * *

ITAM DOCK motif DOCK motif ITAM

hCLASP4 AITKILEVMHTKKRLGLTFRVAFYQGSEFFEEEGKEYTYKEPKLTGLSEISRLRVKIY 1739
hCLASP5 AFDSIVNKDH--KRMFGTYFRVGFYGF--SKFGDLDEQEYFYKEPAITKLPEISHRLEAFY 1750
hCLASP3 AFSKIIVHQTSGWERMFGTYFRVGFYGF--TKFGDLDEQEYFYKEPAITKLAEISHRLEGFY 1872
hCLASP2 -----DFFEDDGKEYTYKEPKLTPLSEISQRLLKIYS 1710
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGFYGF--AHFGDLDEQEYFYKEPSITKLAEISHRLEEFY 1791
hCLASP1 SYLKVAEVVNSEKRLFRGYRVAFYQGSEFFEEEGKEYTYKEPKLTGLSEISQRLLKIYA 1912
* : : :*: ** : * :*: ** *

